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QY 3461 AACAATTGATAGTCTAGATGATGATAAGAACTTACTGATTTTCTTCATGCAACTTA 3428
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QY 3429 GIIIIIAAIAAGGATATATGATAGI 3455
Db 3522 GIIIIIAAIAAGGATATATGATAGI 3548
RESIDUE:
AHK86079
Db AHK86079 standard: cDNA: 4740 BP.
XX
AC AHK86079:
XX
CT G3-SEP-2002 (first copy)
XX
DE Human retinoblastoma protein cDNA sequence.
XX
KW Human retinoblastoma protein; Rb; cyclastatic; cancer; apoptosis;
Rb myeloductone; antisense; breast cancer; bladder cancer; skin cancer;
stomach cancer; liver cancer; colon cancer; oral cavity cancer;
lymphoma; leukemia; gene; ss.
XX
S Hom. sapiens.
XX
EN W 2002-08-01
XX
DE 30 MAY-2002.
XX
EF 24 NOV-2001; 2001W-X2002036.
XX
EF 24 NOV-2000; 2000KR-0070084.
EF 24 DEC-2000; 2000KR-0080184.
XX
FA (B1-3) MENEMIA CO LTD.
XX
EE Lee J.
XX
WP 2002-08-01 50839754.
XX
XX
EF Anticancer agent useful for treatment of cancer and of skin.
XX
XX
ES Example 4; Page 38-42; 44pp; English.
XX
XX
DE The invention relates to an anticancer agent comprising mycolactone.
DE Also included for is an anticancer agent comprising mycolactone and
DE antitumor inhibitors of retinoblastoma (Rb) protein expression. The
DE anticancer agent is used for the treatment of cancers such as breast,
DE bladder, skin, stomach, liver, colon and oral cavity, lymphoma and
DE leukemia. The anticancer agent induces apoptotic death of cancer
DE cells and the Rb inhibitor increases the apoptosis-inducing activity of
DE mycolactone even in Rb positive cancer cells. The agent is specific to
DE cancers in which Rb proteins are optionally expressed and mycolactone
DE shows very strong anticancer effect in Rb positive cancers.
DE The present sequence is the human cDNA for retinoblastoma protein.
XX
SV Sequence 4740 BP; 1508 A; 887 G; 862 C; 1483 T; 0 other;
Query Match 98.8%; Score 3412.8; DB 24; Length 4740;
Best Local Similarity 99.9%; Seed No. 0;
Matches 3439; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
QY 3461 AACAATTGATAGTCTAGATGATGATAAGAACTTACTGATTTTCTTCATGCAACTTA 3428
Db 3462 AATACATTTTCACTACCTCAGATGATGATAAGAACTTACTGATTTTCTTCATGCAACTTA 3521
QY 3429 GIIIIIAAIAAGGATATATGATAGI 3455
Db 3522 GIIIIIAAIAAGGATATATGATAGI 3548

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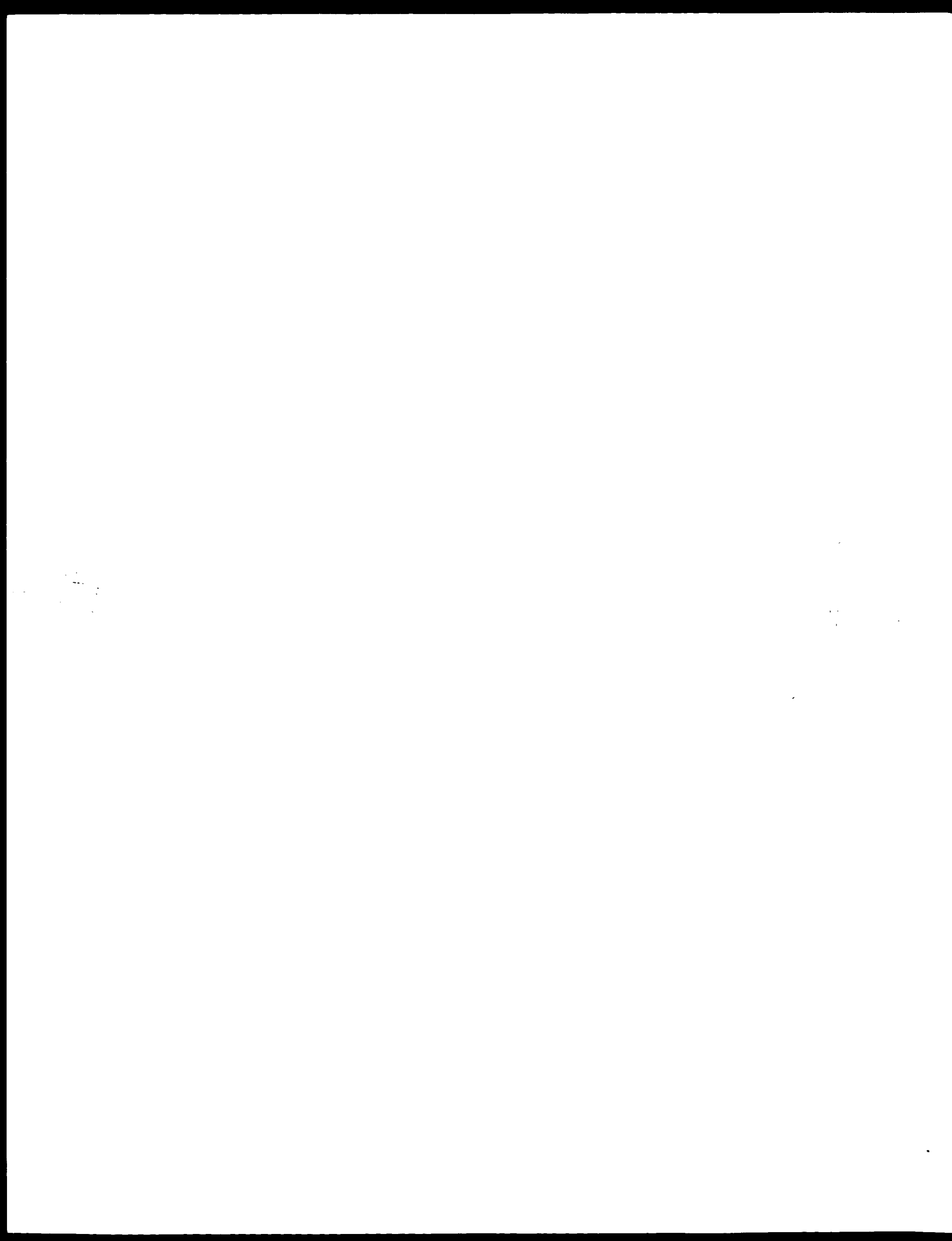
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Db 360 TTGCTTAACTTTGGGCAAAAGTTTCACTGCTGGATGAGTATTGGGAGGTATATATTCAAAA 419
QY 186 CAAAAAGCAATTTGGGCAAAAGTTTCACTGCTGGATGAGTATTGGGAGGTATATATTCAAAA 248
Db 420 GAAAAAGCAATTTGGGCAAAAGTTTCACTGCTGGATGAGTATTGGGAGGTATATATTCAAAA 479
QY 249 GTTCAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 307
Db 480 GTTCAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 538
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QY 428 TGAATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 487
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QY 1088 AATATTTTATAGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1147
Db 1319 AATATTTTATAGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1378
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XX 27 AUG-1998.
 XX 14-FEB-1998; 98WO-USO3041.
 XX 20-FEB-1997; 97US-0038118.
 XX (BAYLOR) BAYLOR COLLEGE MEDICINE.
 XX (TEXAS) UNIV TEXAS SYSTEM.
 XX Benedict WF, Hu S, Xu H, Zhou Y;
 XX WFL: 1998-480788/41.
 XX P PSUB; AAW69367.
 XX Retinoblastoma suppressor protein with N terminal modification -
 XX inhibiting cellular proliferation, particularly cancer
 XX Claim 22; Page 159-162; 249pp, English.
 XX This sequence encodes a modified retinoblastoma tumour suppressor
 XX protein (RbSp) of the invention. The proteins can be used for inhibiting
 XX cellular proliferation, when coadministered with a p53 protein. The RbSp
 XX can be used for treating diseases characterised by abnormal cellular
 XX proliferation, particularly cancers. The RbSp have a broader spectrum of
 XX activity than wild type RbSp.
 XX Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T; 0 other;
 XX
 XX Query Match 95.9%; Score 3315; DB 19; Length 3323;
 XX Best Local Similarity 100.0%; Fwd N. G.
 XX Matches 3315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 XX 469 TTTATTAAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 428
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 XX 429 AATGTAAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
 XX 621 ATATTAAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 680
 XX 489 ATATTAAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
 XX 681 CAG 740
 XX 549 CAG 608

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4004.4	89.8	3242	1 US-08-048-760-1 Sequence 3, Appl
4	4004.4	89.8	3242	1 US-08-048-760-1 Sequence 4, Appl
5	2433.6	72.7	2994	1 US-08-048-760-1 Sequence 5, Appl
6	2433.6	72.7	2994	1 US-08-048-760-1 Sequence 6, Appl
7	2433.6	72.7	2994	1 US-08-048-760-1 Sequence 7, Appl
8	2433.6	72.7	2994	1 US-08-048-760-1 Sequence 8, Appl
9	2433.6	72.7	2994	1 US-08-048-760-1 Sequence 9, Appl
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24	2433.6	72.7	2994	1 US-08-048-760-1 Sequence 24, Appl
25	2433.6	72.7	2994	1 US-08-048-760-1 Sequence 25, Appl
26	2433.6	72.7	2994	1 US-08-048-760-1 Sequence 26, Appl
27	2433.6	72.7	2994	1 US-08-048-760-1 Sequence 27, Appl

28	43.2	1.3	509	4	US-09-352-616A-202	Sequence 202, App
29	43.2	1.3	509	4	US-09-352-616A-202	Sequence 202, App
30	43	1.3	5852	1	US-07-867-106-2	Sequence 2, Appl
31	42.8	1.3	615	4	US-08-998-416-186	Sequence 186, App
32	42.6	1.3	1189	1	US-08-407-591-2	Sequence 2, Appl
33	42.6	1.3	2652	4	US-09-234-827B-3	Sequence 3, Appl
34	42.4	1.3	1186	2	US-08-731-722-5	Sequence 5, Appl
35	42.4	1.3	1776	1	US-08-742-001-29	Sequence 29, Appl
36	42	1.3	665	2	US-08-883-795A-36	Sequence 36, Appl
37	42	1.3	1864	4	US-09-468-265-4	Sequence 4, Appl
38	41.8	1.2	1670	4	US-09-306-060-1	Sequence 1, Appl
39	41.4	1.2	16124	2	US-08-487-826B-14	Sequence 14, Appl
40	41.2	1.2	821	4	US-08-998-416-541	Sequence 541, App
41	41.2	1.2	837	4	US-08-998-416-288	Sequence 288, App
42	41.2	1.2	2030	2	US-08-705-937-7	Sequence 7, Appl
43	40.8	1.2	1144	1	US-08-014-944A-1	Sequence 1, Appl
44	40.8	1.2	1144	1	US-08-486-421-2	Sequence 2, Appl
45	40.8	1.2	1144	1	US-08-470-911-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-048-760-1
Sequence 1, Application US/08038760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Hu, Shi-Xue
TITLE OF INVENTION: Broad spectrum tumor suppressor genes, gene products and
METHOD OF INVENTION: Methods for tumor suppression and therapy.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ponsate & Edwards
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/048,760
FILING DATE: 1999.04.25
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ponsate, Hiram M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025, 909
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 750-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19...2469
US-08-048-760-1

Query Match: 89.8%, Score: 4004.4, DB: 1, Length: 3242;
Best Local Similarity: 100.0%, Prod. No.: 0;
Matches: 3605, Conservative: 0, Mismatches: 1, Gaps: 0;

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QY	402	TAAAGGCAAGTATTAAATAGTCAATCATCTGCTGATTTTCAATTCAGTTAATGCTATG	461
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QY	462	GTGCTTGACATTTTATTAATAACTCTGACCTGCCAGTGTGCTCAAGAGACCATATAAAC	521
DB	345	GTGCTTGACATTTTATTAATAAATCTGACCTGCCAGTGTGCTCAAGAGACCATATAAAC	404
QY	522	AGCTGTTATAGCATTAATGTTGCTGCTGAGAACCTCAGAGGAGCTCAGAACAGAGTGC	581
DB	405	AGCTGTTATAGCATTAATGTTGCTGCTGAGAACCTCAGAGGAGCTCAGAACAGAGTGC	464
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QY	1122	TGATACAGAGTATAAAGCTTGAGCTTGCCTGTATTACCGAGTATGGAATCATGCT	1181
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DB	1065	TAAATCAGAGAGAGAGTATATCAATCAAAATTTTACCAACTCTGATGATCAACAAT	1124
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DB	1185	TATATCTCAATCTGATCTCGAAGCAATTTGCTTTTCTTTCCATCATCTCGAATGCT	1244
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QY	1902	CCAAATATGATCTGTTCATGATATGATATATGATATATAGATATGATATAGCTGGCTTAAAT	1961
DB	1785	CCAAATATGATCTGTTCATGATATGATATATGATATATAGATATGATATAGCTGGCTTAAAT	1844
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DB	1905	TGTTTTCATCAAGAAAGCAAGATAGATATATGATATATAGATATGATATAGCTGGCTTAAAT	1964
QY	2082	GCAGACACTCAAAACAAATATTTTCGACTATGCTTCCACAGCGCGCTTACCTTGCTGTCAC	2141
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RESULT 4
 US 08 470 091 1
 Sequence 1, Application US/084/20091
 Patent No. 5912246
 GENERAL INFORMATION:
 APPLICANT: Xu, Hong Ji
 APPLICANT: Hu, Shi Xue
 APPLICANT: Benedict, William F.
 TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and
 METHODS FOR Tumor Suppressor Gene Therapy.
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESS: Penrose & Edmunds
 STREET: 1155, Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10046, 2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,091
 FILING DATE: JUN 16, 1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/06/048,760
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Foussant, Brian M
 REGISTRATION NUMBER: 28,462
 REFERENCE NUMBER: 7439, 525, 939
 TELEPHONE: (212) 790, 9090
 TELEFAX: (212) 869, 9741/8864
 INFO: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4242 base pairs
 TYPE: nucleic acid
 STRANDNESS: double
 TOPOLOGY: not relevant
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 19...2469
 US 08 470 091 1

Query Match: 89.8% Score: 3094.4 DB 2: Length: 3232;
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[illegible]

1 RESUB 1 4
 2 US-00-001 092 3
 3 Software 3, Application US/08801092
 4 Patent No. 6074850
 5
 6 GENERAL INFORMATION:
 7
 8 APPLICANT: Antelman, Douglas
 9 APPLICANT: Gregory, Richard J.
 10 APPLICANT: Wills, Kenneth N.
 11
 12 TITLE OF INVENTION: Tissue Specific Expression of
 13 TITLE OF INVENTION: Retinoblastoma Protein
 14
 15 NUMBER OF SEQUENCES: 46
 16
 17 CORRESPONDENCE ADDRESS:
 18 ADDRESSEE: TOWNSEND AND TOWNSEND and CREW LLP
 19 STREET: TWO Embarcadero Center, 8th Floor
 20 CITY: San Francisco
 21 STATE: CA
 22 COUNTRY: USA
 23 ZIP: 94111
 24
 25 COMPUTER READABLE FORM:
 26 MEDIUM TYPE: Floppy disk
 27 COMPUTER: IBM PC compatible
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 29 CREATING SYSTEM: PC/IOS/MS-DOS
 30 SOFTWARE: Patent In Release #1.0, Version #1.30
 31 SCREEN APPLICATION DATA:
 32 APPLICATION NUMBER: US2087601 092

FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09 08/751,517
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FITTS, REXCE A.
REGISTRATION NUMBER: 35,146
REFERENCE/DOCKET NUMBER: 016930-001020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
OS-08-801-092-3

[illegible]

LENGTH: 2995 base pairs
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 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
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 LOCATION: 133..2925
 OTHER INFORMATION: /product= "Rb"
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 SEQUENCE DESCRIPTION: SEQ ID No: 7:
 US 09 428 674A 7

Query Match: 72.4% Score: 2429.2 DB: 4 Length: 2995;
 Best local Similarity: 92.7% Pred. No. 0;
 Matches: 2446; Conservative: 0; Mismatches: 3; Indels: 207; Gaps: 1;

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1 NUMBER OF SEQUENCES: 4
2
3 CORRESPONDENCE ADDRESS:
4 ADDRESSSES: Temple University of the Commonwealth
5 ADDRESSSES: System of Higher Education
6 STREET: 406 University Services Building
7 CITY: Philadelphia
8 STATE: Pennsylvania
9 COUNTRY: U.S.A.
10
11 ZIP: 19122
12
13 COMPILER REALABLE FORM:
14 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
15 COMPILER: IBM PS/2
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17 OPERATING SYSTEM: MS DOS
18
19 SOFTWARE: WordPerfect 5.1
20
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US-99-019 49A
23 FILING DATE: August 12, 1993
24
25 CLASSIFICATION: 435
26
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER:
29 FILING DATE:
30
31 AGENCY/AGENT INFORMATION:
32 NAME: Mullins, J.G.
33 REGISTRATION NUMBER: 43,073
34 REFERENCE/BOOKET NUMBER: 6056-188
35
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (215) 568-8383
38 TELEFAX: (215) 568-5549
39 TELE: No. 54570496
40
41 INFORMATION FOR SEQ ID NO: 1:
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43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 949 base pairs
45 TYPE: nucleic acid
46 STRANDEDNESS: Single
47 TOPOLOGY: Linear
48
49 US-98 106, 49A 1

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RESULT 4

US-09-315-1113-3

Sequence 3, Application US/09315113

Patent No. 6379927

GENERAL INFORMATION:

APPLICANT: Antelman, Douglas

Gregory, Richard J.

Wills, Kenneth N.

TITLE OF INVENTION: Tissue Specific Expression of

Receptor Protein

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-Linux/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/315,113

FILING DATE: 10-May-1999

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/801,092

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136


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66 2359 GATATATATATATATATATATATATATATATATATATATATATATATATATAT 2418
69 692 MetGlnArgLeuLysThrAsnIleLeuIleTyrAlaSerThrAlaProThrLeuSer 711
72 2419 ATGACAGACATGAAATATATATATATATATATATATATATATATATATATAT 2478
75 712 ProLeuProHisIleThrAlaSerProLysPheProSerSerProLeuAlaGluPro 731
78 2479 GATATATATATATATATATATATATATATATATATATATATATATATATATAT 2538
81 732 GlyPheAsnIleTyrLeuSerProLysSerProTyrLysIleSerGluCysLeuPro 751
84 2539 GATATATATATATATATATATATATATATATATATATATATATATATATATAT 2598
87 752 TTTProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheCly 771
90 2599 ATACCAATATATATATATATATATATATATATATATATATATATATATATATAT 2658
93 772 ThrSerGluLysPheGlnLysIleAsnIleMetValCysAsnSerAspArgValLeuLys 791
96 2659 ATTTGAGAAATTCATATATATATATATATATATATATATATATATATATATAT 2718
99 792 ATGSerAlaGluGlySerAspProLysProLysLysLysLysLysLysLysLys 811
102 2719 AGAAGTCTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 2778
105 812 GlySerAspGluAlaAspLeuSerLeuPheTyrLysValTyrAlaValTyrLeu 831
108 2779 GATATATATATATATATATATATATATATATATATATATATATATATATATAT 2838
111 832 LeuAlaLeuMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 851
114 2839 GATATATATATATATATATATATATATATATATATATATATATATATATATAT 2898
117 852 AspIleSerAsnLysGluGluLys 859
120 2899 GATATATATATATATATATATATATATATATATATATATATATATATATATAT 2922
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REMARKS

US-09-026-459 7

SEQUENCE 7

Patent No. 5,932,210

GENERAL INFORMATION

APPLICANT: Gregory, Richard J.

INVENTOR: Willis, Fred N.

```
3 APPLICANT: Maneval, Daniel C.
4 TITLE OF INVENTION: Recombinant Adenoviral Vector and
5 METHODS OF USE
6 NUMBER OF SEQUENCES: 9
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Campbell and Flores
9 STREET: 4370 La Jolla Village Drive, Suite 700
10 CITY: San Diego
11 STATE: California
12 COUNTRY: USA
13 ZIP: 92122
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patent in Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US-09-026-459, 638
21 FILING DATE:
22 CLASSIFICATION:
23 PRIORITY APPLICATION DATA:
24 APPLICATION NUMBER: US-08-328,673
25 FILING DATE: 25-OCT-1994
26 APPLICATION NUMBER: US-08-233,777
27 FILING DATE: 19-MAY-1994
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US-08-0142,669
30 FILING DATE: 25-OCT-1993
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Campbell, Cathryn A.
33 REGISTRATION NUMBER: 31,815
34 REFERENCE/DOCKET NUMBER: P-CJ 1192
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (619) 535-9001
37 TELEFAX: (619) 535-8949
38 INFORMATION FOR SEQ ID NO: 7:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 2995 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44 FEATURE:
45 NAME/KEY: CDS
46 LOCATION: 139..2922
47 US-08-959-638-7
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Alignment Scores:

Pred. No.:	0	Length:	2995
Score:	4401.50	Matches:	858
Percent Similarity:	92.46%	Conservative:	0
Best local Similarity:	92.46%	Mismatches:	1
Query Match:	98.84%	Indels:	69
DB:	2	Gaps:	1

US-08-959-638-7 (1-2995) X US-08-959-638-7 (1-2995)

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37 1 MetProProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAlaAlaAlaPro 20
38 139 ATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 198
39 21 PheValPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 40
40 199 CCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 258
41 41 AspLeuProLeuValThrArgGluThrPheGluGluThrGluGluProAspPheThrAlaLeu 40
42 259 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 418
43 61 CysCysLysSerLeuLysIlePheAsnValAlaIleAlaIleAlaIleAlaIleAla 80
44 319 TGTCAAAATTAACATATACATATACATATACATATACATATACATATACATATACAT 478
45 81 ValSerSerValAspSerValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
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[illegible]

1080 AAAATTGAGGTTGGTGGTATACCGAGTAATGGAAATCAATGCTTAAATCAGAACAGAA 1080
 417 ArdeLeuSerThrLeuAsnPheserLysLeuAsnAspAsnIlePheIleMetSerLeu 417
 1140 GAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 437 LeuAlaCysAlaLeuGluValMetAlaThrThrSerArgSerThrSerGlnAsnLeu 437
 1200 TTGGGCTGAGGCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 457 AsnSerArgThrAspLeuSerThrProTyrIleLeuAsnValLeuAsnLeuLysAlaPhe 457
 1260 GATTCGAGAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
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 1440 GAT 1440
 537 GluSerAlaCysProLeuAsnLeuProLeuGlnAsnHisThrAlaAlaAspMetLys 537
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 1560 GTTCTGCTGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
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 1620 AATGACACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 597 LeuSerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCys 597
 1680 GTTCAATGTTTATATAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 617 GluArgLeuLeuSerGluHisThrGluLeuGluHisIleIleThrLeuPheGluHis 617
 1740 GAAAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 637 ThrLeuGluAsnGluTyrGluLeuMetAlaArgAspArgHisLeuAspGluIleMetMetCys 637
 1800 AATGAT 1800
 657 SerMetTyrGlyIleGlyValLysAsnIleAspLeuLysPheLysIleIleValThr 657
 1860 TATATGAT 1860
 677 AlaTyrLysAspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLysGlu 677
 1920 GATAAAGAT 1920
 697 GluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetGluAlaLeuLysThr 697
 1980 GAGAT 1980
 717 AsnIleLeuGlnTyrAlaSerThrArgProThrLeuSerProIleProHisIlePro 717
 2040 AATATTTGAT 2040
 737 ArgSerProTyrLysPheProSerProLeuArgIleProGlyGlyAsnIleTyrIle 737
 2100 GAAGGCTGAT 2100
 757 SerProLeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThr 757
 2160 TACCGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160

QY 758 ProArgSerArgIleLeuValSerIleClyClySerPheClyThrSerGlyLysPheCly 777
 DB 2161 CCAAGATCAAGATATTTAGTATCAATTTGTAATCAATTTGTAATCAATTTGTAATCAATTTGTA 2220
 QY 778 TGTTCASGCTCCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
 DB 2221 AATAATATATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
 QY 798 AsnProPheLysPheLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 817
 DB 2281 AATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2440
 QY 818 GlySerLysHisLeuProClyClySerLysPheClyClyClyClyClyClyClyClyClyCly 837
 DB 2341 GAAATGATAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
 QY 838 ThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGlu 857
 DB 2401 ACTCGAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
 QY 858 GluLys 859
 DB 2461 GAGAAA 2466

RESULT 10

US-08-038-760-2/C
 ; Sequence 2, Application us/08038760
 ; Patent No. 5496731
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Hong-Ji
 ; APPLICANT: Hu, Shi-Xue
 ; APPLICANT: Benedict, William F.
 ; TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
 ; TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Pennic & Edmonds
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/038,760
 ; FILING DATE: 19940325
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Poissant, Brian M
 ; REGISTRATION NUMBER: 28,462
 ; REFERENCE/DOCKET NUMBER: 7409-025-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 222 base pairs
 ; TYPE: NUCLEIC ACID
 ; STRANDEDNESS: double
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: DNA
 US-08-038-760-2

Alignment Scores:
 Seq. No. 6 Length: 4242
 Score: 3858.50 Matches: 757
 Percent Similarity: 91.70% Conservative: 12


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193 ValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAlaArg 194
194 313 JACIIIAACGGTCTICCAACAGCCACCCICG----- 342
195 IleAlaIleGlnLeuGlnAsnAspThrArgGileIleGluValIleCysGlyHisGlu 213
196 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999

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QY 361 ArgValLeuIleLysGluGlnIleProSerSerIleValPheTyrAsnSerValPhe 740
DB 362 CGTCTTTTCATCAACAGAGGAGTATGATCTATTATAGTATCTATTAACCTGGCTTC 2418
QY 761 MetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProPheIleLeuSer 780
DB 762 ATGCAAGAGATCGAAGAAATATTTTTCAGTATGCTTCACAGGAGGAGGATCTTCTCA 2478
QY 781 ProIleProHisIleProArgSerProTyrIleLysPheProSerProLeuArgIlePro 800
DB 782 CCAATACCTTCACATCTCTCAAGCCCTTACAAAGTTTCTTACCTACCTTACGCAATGCT 2538
QY 801 GlyGlyAsnGlyGlyGlySerPheLeuLysSerIleLeuIleSerIleLeuLeuLeu 820
DB 802 GAACTCAATATGCTATATATCACTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2598
QY 821 ThrProThrIleMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheIle 840
DB 822 ACATCAATCAAAATATGCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2658
QY 841 ThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLys 860
DB 842 ACTCTGAGAGAGCTTCAGAAAATAATATCAATGATGATGATGATGATGATGATGATGATGAT 2718
QY 861 ArgSerAlaGlySerArgProPheLysProLeuLysLysLeuArgPheAspIleGlu 880
DB 862 AGAAGTCTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2778
QY 881 GlySerAspGluAlaAspGlySerLysHisIleLeuProGlyGluSerLysPheGlnLys 900
DB 882 GGAATCATGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2838
QY 901 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAspSerMet 920
DB 902 CTCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2898
QY 921 AspThrSerAsnLysGluGlnLys 928
DB 922 CATACCTCAACCAACCAACCAAGAA 2922
RESULT 4
US-09-315-113-3
Sequence 3, Application US/09315113
Patent No. 6379927
GENERAL INFORMATION:
APPLICANT: Autelman, Douglas
Gregory, Richard J.
Wills, Kenneth W.
TITLE OF INVENTION: Tissue Specific Expression of
Retinoblastoma Protein
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,113
FILING DATE: 19-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,092
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136

QY 361 ArgValLeuIleLysGluGlnIleProSerSerIleValPheTyrAsnSerValPhe 740
DB 362 CGTCTTTTCATCAACAGAGGAGTATGATCTATTATAGTATCTATTAACCTGGCTTC 2418
QY 761 MetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProPheIleLeuSer 780
DB 762 ATGCAAGAGATCGAAGAAATATTTTTCAGTATGCTTCACAGGAGGAGGATCTTCTCA 2478
QY 781 ProIleProHisIleProArgSerProTyrIleLysPheProSerProLeuArgIlePro 800
DB 782 CCAATACCTTCACATCTCTCAAGCCCTTACAAAGTTTCTTACCTACCTTACGCAATGCT 2538
QY 801 GlyGlyAsnGlyGlyGlySerPheLeuLysSerIleLeuIleSerIleLeuLeuLeu 820
DB 802 GAACTCAATATGCTATATATCACTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2598
QY 821 ThrProThrIleMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheIle 840
DB 822 ACATCAATCAAAATATGCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2658
QY 841 ThrSerGluLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLys 860
DB 842 ACTCTGAGAGAGCTTCAGAAAATAATATCAATGATGATGATGATGATGATGATGATGATGAT 2718
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DB 862 AGAAGTCTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2778
QY 881 GlySerAspGluAlaAspGlySerLysHisIleLeuProGlyGluSerLysPheGlnLys 900
DB 882 GGAATCATGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2838
QY 901 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAspSerMet 920
DB 902 CTCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2898
QY 921 AspThrSerAsnLysGluGlnLys 928
DB 922 CATACCTCAACCAACCAACCAAGAA 2922

1 REFERENCE/BLANKET NUMBER: 016940-001020

2 TELECOMMUNICATION INFORMATION:

3 TELEPHONE: 415 576 0200

4 TELEFAX: 704 576 0400

5 INFORMATION FILE SEQ ID NO: 4

6 SEQUENCE CHARACTERISTICS:

7 LENGTH: 2094 base pairs

8 TYPE: nucleic acid

9 STRANDEDNESS: single

10 TOPOLOGY: linear

11 MOLECULE TYPE: cDNA

12 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

58 09 415 114 3

Alignment Scores:

3000 0 4767.00 2994

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1699 CTTAAATTAAGAGGCTTTCATTTTATCAAAAGTATCGAAAGCTTTATCAAAAGCAGAAAGC 1758
541 AsnLeuThrArgGluMetIleTyrLysHisLeuGluArgTyrGlnIleAspIleMetGluSer 560
1759 AACTTGAACAGAGAAATCAIAAAATATTAAGACGATGCAACATCGCAATCAATGCAATCC 1818
561 LeuAlaIleProLeuSerProGluPheAspLeuIleTyrGlnSerLysAspArgIle 580
1819 CTTCATGATGCTTCTAGATATATCTTATTTATTTATTAATTAATTAATTAATTAATTAATTA 1878
581 GlyProThrAspHisLeuGlnSerAlaCysProLeuAsnLeuProLeuGlnAsnAspHis 600
1879 GGAATTAATGATCAATGAAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1948
601 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLeuLysLysGlySerThrThr 620
1949 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1998
621 ArgValAspSerThrAlaAsnAlaGlnIleGlnAlaThrSerAlaPheGlnThrGlnLys 640
1999 GGTGTTAAATTTCTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 2058
641 ProLeuLysSerThrSerLeuSerLeuPheIleTyrLysLysValTyrArgLeuAlaTyrLeu 660
2059 CATTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2118
661 ArgLeuAsnThrLeuGlySerArgLeuLeuSerGlnHisProIleLeuGlnHisIleIle 680
2119 GGGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2178
681 TrpThrLeuPheGlnHisThrLeuGlnAsnGlnIleTyrIleLeuMetArgAspArgHisLeu 700
2179 TGGATGCTTTTCCAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2248
701 AspIleMetMetCysSerMetTyrGlyIleCysTyrValLysAsnIleAspLeuLys 720
2249 CACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2298
721 PheLysIleValThrAlaTyrLysAspLeuProHisAlaValGlnIleThrPheLys 740
2299 TCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2358
741 ArgValLeuIleTyrGlnHisLeuThrArgSerThrIleValPheTyrAsnSerValPhe 760
2359 GGTGTTTTCATGAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2418
761 MetGlnArgLeuLysThrAsnIleLeuGlnIleTyrAlaSerThrArgProThrLeuSer 780
2419 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2478
781 ProIleProIleIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 800
2479 GATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2538
801 GlyLysAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerIleCysLeuPro 820
2539 GGAAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2598
821 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleCysLeuSerPheCys 840
2599 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2658
841 ThrSerGlnLysPheGlnLysIleAsnGlnMetValTyrLysAsnSerAspArgValLeuLys 860
2659 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2718
861 ArgSerAlaIleGlnGlySerAsnProProLysProLysIleLysLeuArgPheAspIle 880
2719 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2778
881 GlyArgPheAlaAspLysSerLysHisLeuProGlnLysSerPheGlnGlnLys 900

Db 2779 GCATCATCAAGTACAGTAAAGTAAACAATGTCAGACAGATGCTAAATTTTCAGTACAAA 2838
QY 901 LeuAlaIleMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 920
Db 2839 CTGCGAAGAAATGATTTCTAGTCAAGACGGAATGCAAAAGTAAAGAAATGATGATGATG 2898
QY 921 AspThrSerAsnLysGlnLysLys 928
Db 2899 GATACCTCAAAATAGAAAGTAAAGAA 2922
RESULT 8
US-08-038-760-1
: Sequence 1, Application US/08048760
: Patent No. 5496731
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong-li
: APPLICANT: Hu, Shi Xue
: APPLICANT: Benedict, William F.
: TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and
: METHODS OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Peptide & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10046-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/048,760
: FILING DATE: 19930325
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 7409-025-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790,9090
: TELEFAX: (212) 869,9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3232 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 19..2469
US-08-038-760-1
Alignment Scores:
Pred. No.: 0 Length: 3232
Score: 4203.00 Matches: 818
Percent Similarity: 99.88% Conserved: 1
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 87.60% Indels: 0
DB: 1 Gaps: 0
US-09-026-459A-51 (1 928) x US-08-048-760-1 (1 3232)
QY 109 ASPLeuLysAspMetSerPheThrPheThrGlnLeuGlnLysAsnIleCysVal 128
Db 7 GACTACATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 66
QY 129 HisLysPhePheAsnLeuGlnLysGlnIleAspThrArgThrLysValAspAsnAlaMet 148

QY 809 ProlyserProteinLysylSerThrGluAspThrGluLysSerAspGluAlaAspGlySer 888
 DB 2287 CTTAAAGACTGAAAAAATACGGTTTGATATTGAAGATCAGATGAAGCAGATGAAGT 2346
 QY 889 LysHisLeuProGlyGlySerLysPheGluLysLeuAlaGluMetThrSerThrArg 908
 DB 2347 AAAATGCGAGAGAGAGTAAATTCAGCAAAATGGCAGAAATGACCTGTACTCGA 2406
 QY 909 ThrArgMetGlyGlyGlyGlyMetAlaAspSerMetAspThrSerAsnLysGluLys 928
 DB 2407 AACCAATGCAAAATGCAATGATAGATGATGATCTCAAAACAGGGAAGAGAAA 2466

RESULT 9

US 09 026 459a-51

Sequence 2: Application US/09048760

Patent No. 6496741

GENERAL INFORMATION:

APPLICANT: Xie, Renyi Li

APPLICANT: Renyi, Shi Xue

TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and

METHODS FOR Tumor Suppressor Gene Therapy.

NUMBER OF SEQUENCES: 3

COMPRESSION: AUCPSS: 3

ADDRESSER: Institute & Edwards

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10046-2711

COMPUTER RELEASABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-PC/MS-PC/5

SOFTWARE: Patent In Release #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/048,760

FILING DATE: 1999.04.25

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Perissian, Brian M

REGISTRATION NUMBER: 28,412

REFERENCE NUMBER: 7409-025-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-0090

TELEFAX: (212) 865-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4242 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

RELEVANCE: not relevant

MOLECULE TYPE: DNA

US 09 026 459a-51

Alignment Score:

Prod. No.: 0 Length: 4242

Sequences: 4204.00 Matches: 818

Percent Similarity: 99.80% Conservativity: 1

Best Local Similarity: 99.79% Mismatches: 1

Query Match: 87.60% Indels: 0

Gaps: 0

US 09 026 459a-51 (1-928) x US 09 048 760 2 (1-4242)

QY 109 AspGluGlyAspMetSerPheThrGluGluThrGluLysAsnThrGluThrSerVal 128
 DB 4240 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3171
 QY 129 HisLysPhePheAsnLeuLeuLysGluThrSerThrLysValAspAsnAlaMet 148
 DB 4170 CATAAATGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 3111

QY 149 SerArgLeuLeuLysLysLysValLeuPheAlaLeuLeuSerLysLeuGluArgThr 168
 DB 3110 TCAGACAGTGTGAAGAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 4051
 QY 169 CysGluLeuLeuLeuLeuThrGluProSerSerSerLysSerThrGluLeuLeuAsnSerAla 188
 DB 4050 TGTCAACTATATATATTCAC 2491
 QY 189 LeuValLeuLysValSerThrPheThrPheLeuLeuAlaLysSerLysValLeuLeuMet 208
 DB 2990 TTGGTGTAAAGAGTTCCTGATTCACACATTTTATTAAGTAAAGGGAAGATTAACAAATG 2931
 QY 299 GlnAspPheLeuValLeuSerPheLeuLeuMetThrLysValLeuAlaPhePheLys 228
 DB 2930 GAAGATGATCTGGTGATTCATTTCATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2871
 QY 229 LeuSerProProMetLeuLeuLysGluPheThrAlaValLeuThrThrLeuAsnGly 248
 DB 2870 CTCAC 2811
 QY 249 SerProArgThrProAlaArgGluLeuAsnArgSerAlaArgLeuAlaLysGluLeuLeu 268
 DB 2810 TCACCTGAC 2751
 QY 269 AsnAspThrArgThrLeuLeuValLeuLysGluLysGluLysGluLysAsnThrAspGluVal 288
 DB 2750 AATGATACAGCAATTTATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2691
 QY 289 LysAsnValThrPheGlySerPheLeuProGluMetAsnSerLeuGlyLeuValThrSer 308
 DB 2690 AAAAATGTTTATTTCAAAAATTTATATATTTTATGAAATTCCTCTGCAATTCGAAATCT 2831
 QY 309 AsnGlyLeuProGluValThrGluLeuSerLysArgThrGluGluGluGluGluGluGlu 328
 DB 2630 AATGGACATCCACAGCTTGAAGAACTTTCGAAAGTAAAGTAAAGTAAAGTAAAGTAA 2571
 QY 329 LysAspPheAspAlaArgLeuPheLeuAspHisAspLysThrLeuGluThrAspSerLle 348
 DB 2570 AAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2511
 QY 349 AspSerPheGluThrGluArgThrProArgLysSerAsnLeuAspGluLeuValAsnVal 368
 DB 2510 CACAGCTTTCGAAAC 2451
 QY 369 ThrProProHisThrProValArgThrValMetAsnThrThrLeuLeuLeuMetLle 408
 DB 2450 ATTCTTCAC 2491
 QY 389 LeuAsnSerAlaSerAspGluProSerGluAsnLeuLeuSerLysPheAsnAspLysThr 408
 DB 2390 TTAAATTCAGGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2441
 QY 409 ValAsnProLysGluSerThrLeuLysArgValLysAspThrGlyThrGluPheGlu 428
 DB 2340 GCGAAATCCAAAGAGAAATATATGAAAGAGATGAAAGATATGAAAGATATGAAAG 2271
 QY 429 LysPheAlaLysAlaValGluGluGluGluGluGluGluGluGluGluGluGluGlu 448
 DB 2270 AAAATTCGAAAG 2211
 QY 449 GlyValAlaGluGlyThrArgValMetGluSerMetLeuLysSerGluGluThrArg 468
 DB 2210 GAGGTGCTTGTATTATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2151
 QY 469 SerThrGluAsnPheSerLysLeuLeuAsnAspAsnThrGluHisMetSerLeuLeuAla 488
 DB 2150 TCCATTCACAAAATTTAGTAAATTTTCGAAATGCAACAAATTTTCATATATATATATAT 2091
 QY 489 CysAlaLeuGluValValMetAlaThrThrLysSerArgSerThrSerGluAsnLeuAspSer 508
 DB 2090 TCCGCTCTTGAGCTGTAATGCTGACATATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2031

100 7 CACCTACAGACACAGCGCGCTTAACTTCTTACAGCAACACACAGCAAAACACACAGCACTGTC 66
 129 HSTLSTSPhePheAsnLeuLeuLeuLysGluIleAspThrSerThrLysValAspAsuAlaMet 148
 167 CATAAATTTCTTAACTTAAATAAAATTAATGAGTACAGTACCAATGATGATGATGATG 126
 149 SerArqLeuLeuLysLysPheAspValLeuPheAlaLeuPheSerLysLeuGluArqThr 168
 127 PAAAGACGTTGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 146
 169 CysGluLeuLeuIleThrProSerSerSerIleSerThrGluIleAsnSerAla 188
 187 LSTAACTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 216
 189 LeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGluIleValLeuGluMet 208
 247 LGGGTGTAAAGGTTCTTGATACATTTTATTAATTAATTAATTAATTAATTAATTAATTA 306
 209 GluAspAspGluValIleSerPheGluLeuMetLeuCysValLeuAspTrpPheLeuLys 228
 307 GAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 366
 229 LeuSerProProMetLeuLeuLysGluProTrpLysThrAlaValIleProIleAsnGly 248
 367 CTTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426
 249 SerProArqThrProArqArqGluGluAsuArqSerAlaArqIleAlaLysGluLeuGlu 268
 427 PAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAA 486
 269 AsnAspThrArqIleLeuLeuValLeuCysLysGluIleSerLysAsnIleAspGluVal 288
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 289 LysAsnValTrpPheLysAsuPheIleProPheMetAsnSerLeuLeuLysLeuValThrSer 308
 547 AAAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 606
 309 AsnGlyLeuProLeuValIleLeuLeuSerLysArqTrpGluIleTrpLeuLysAsn 328
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 329 LysAspLeuAspAlaArqLeuPheLeuAspGluAspLysThrLeuGluThrAspSerIle 348
 667 AAAT 726
 349 AspSerPheGluThrGluArqThrProArqLysSerAsnLeuAspGluGluValAsnVal 368
 727 CAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAA 786
 369 IleProProIleThrProValArqThrValMetAsuThrIleGluGluLeuMetIle 388
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 389 LeuAsuSerAlaSerAspLeuProSerGluAsnLeuIleSerTrpPheAsnLysThr 408
 847 TAAATTTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAG 906
 409 ValAsnProLysGluSerIleLeuLysArqValLysAspIleLysIlePheLysGlu 428
 907 CTAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAGTGTAAAG 966
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US-08-842-883-1
: Sequence 1, Application US/08842884
: Patent No. 5807681
: GENERAL INFORMATION:
: APPLICANT: Giordano, Antonio
: APPLICANT: Baldi, Alfonso
: TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
: NUMBER OF SEQUENCES: 115
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SEIDEL, GONIA, LAVOGENA & MINATO, P.O.
: STREET: Suite 1800 Two Penn Center Plaza
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.0
: APPLICATION NUMBER: US/08/842-883
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Monaco, Daniel A
: REGISTRATION NUMBER: 30,480
: REFERENCE/DOCKET NUMBER: 8421-13 US1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-8384
: TELEFAX: (215) 568-5549
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4853 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 70...3489
US-08-842-883-1
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Score: 837.00 Matches: 295
Percent Similarity: 48.42% Conservative: 173
Best local Similarity: 21.22% Mismatches: 466
Query Match: 17.44% Indels: 484
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US-09-026-459A 51 (1-928) x US-08-842-883 1 (1-4853)

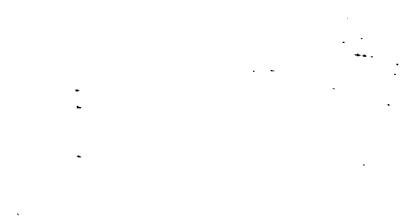
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US-07-708-962-1
Sequence 1, Application US/07708962
Patent No. 5262321
GENERAL INFORMATION:
APPLICANT: Eweb, Mark E.
APPLICANT: Eweb, Mark E.
TITLE OF INVENTION: Tumor Suppressor
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Choate, Hall & Stewart
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07708, 962
FILING DATE: 19910541
CLASSIFICATION: 4.45
ATTORNEY/AGENCY INFORMATION:
NAME: Kennedy, Bill
REGISTRATION NUMBER: 33,407
REFERENCE/DOCKET NUMBER: DPCI 209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5920
TELEFAX: (617) 227-7566
TELEX: 289374
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2808 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO


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14 2407 CAATAAGAGGATGCTGATACACTGCTGCTTTTCCACATATTAAACAACAG----- 2517
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24 2719 GAATGGGCTGGCAAA 2733
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Job time : 164.79 secs



Genware version 5.1.3
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Run on: January 18, 2003, 04:12:19 : Search time 51.9267 Seconds
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Filter: US 09 026 459A 41

Perfect score: 4031

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Ygap 10.0 : Ygapext 0.5
Zgap 6.0 : Zgapext 7.0
Bgap 6.0 : Bgapext 7.0

Searched: 441362 seqs, 15338881 residues

Total number of hits satisfying chosen parameters: 882724

Minimum db seq length: 0

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Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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LOGEXT: 0 - UNITS: bits START: 1 - END: 1 - MATRIX: blosum62 - TRANS: human40.cdi
LIST: 45 - LOCAL: 200 - THR_SCORE: pct - THR_MAX: 100 - THR_MIN: 0 - ALIGN: 15
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WARN: LMP001-40 - THREADS: 1 - XGAP: 10 - XGAPEXT: 0.5 - ZGAP: 6 - ZGAPEXT: 7
YGAP: 10 - YGAPEXT: 0.5 - Bgap: 6 - BgapEXT: 7 - DELEX: 1-7

Database: Issued Patents NA:

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7: 09 026 459A 41

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4605.5	99.4	2994	US 08 204-429-2	Sequence 2, Appl
2	4605.5	99.4	2994	US 08 492-627-4	Sequence 4, Appl
3	4605.5	99.4	2994	US 08 801-092-4	Sequence 3, Appl
4	4605.5	99.4	2994	US 09 315-113-4	Sequence 3, Appl
5	4605.5	99.4	2994	US 08 959-648-7	Sequence 7, Appl
6	4605.5	99.4	2994	US 08 959-648-7	Sequence 7, Appl
7	4605.5	99.4	2994	US 08 959-648-7	Sequence 7, Appl
8	4605.5	99.4	2994	US 08 959-648-7	Sequence 7, Appl
9	4605.5	99.4	2994	US 08 959-648-7	Sequence 7, Appl
10	4605.5	99.4	2994	US 08 959-648-7	Sequence 7, Appl
11	4605.5	99.4	2994	US 08 959-648-7	Sequence 7, Appl
12	4605.5	99.4	2994	US 08 959-648-7	Sequence 7, Appl

13	813.5	17.6	4853	2	US 08 842 877 1	Sequence 1, Appl
14	768	16.6	2898	1	US 07 708 962 1	Sequence 1, Appl
15	763	16.5	2808	2	US 08 152 7218 1	Sequence 1, Appl
16	745.5	16.1	4249	1	US 08 106 494A 1	Sequence 1, Appl
17	745.5	16.1	4249	1	US 08 429 264 1	Sequence 1, Appl
18	516.5	11.2	3747	4	US 09 213 2940 2	Sequence 2, Appl
19	161.5	3.5	10136	5	US 08 453 700-2	Sequence 2, Appl
20	161.5	3.5	10136	5	US 08 453 700-2	Sequence 2, Appl
21	157.5	3.4	8789	1	US 08 428 254 5	Sequence 5, Appl
22	156	3.4	6774	4	US 09 166 450-27	Sequence 27, Appl
23	155.5	3.4	3763	1	US 07 792 865D 1	Sequence 1, Appl
24	154.5	3.3	4868	1	US 08 149 937 12	Sequence 12, Appl
25	154.5	3.3	4868	5	US 08 11310 12	Sequence 12, Appl
26	151	3.3	5293	1	US 08 592 125 54	Sequence 54, Appl
27	151	3.3	5293	2	US 08 687 080-44	Sequence 44, Appl
28	150.5	3.2	4593	4	US 09 404 627 3	Sequence 3, Appl
29	150.5	3.2	4205	4	US 09 404 627-1	Sequence 1, Appl
30	146	3.2	5661	4	US 08 948 105 2	Sequence 2, Appl
31	148.5	3.0	3883	1	US 08 468 036 33	Sequence 33, Appl
32	148.5	3.0	3883	2	US 08 476 843 33	Sequence 33, Appl
33	148.5	3.0	3884	4	US 09 541 782-3	Sequence 3, Appl
34	148.5	3.0	3884	4	US 09 743 820-3	Sequence 3, Appl
35	147.5	3.0	8473	4	US 09 172 422-2	Sequence 2, Appl
36	137	3.0	5181	1	US 08 257 074 10	Sequence 10, Appl
37	134.5	2.9	3393	4	US 09 104 324B 1	Sequence 1, Appl
38	134.5	2.9	3393	4	US 09 162 713-1	Sequence 1, Appl
39	131	2.8	2415	4	US 09 134 001C 2481	Sequence 2481, Ap
40	129.5	2.8	1885	4	US 08 477 831C-9	Sequence 9, Appl
41	129.5	2.8	1885	4	US 08 477 831C-9	Sequence 9, Appl
42	129.5	2.8	2968	4	US 08 477 831C-13	Sequence 13, Appl
43	129.5	2.8	3044	4	US 08 477 831C-12	Sequence 12, Appl
44	128	2.8	1821	4	US 08 477 831C-1	Sequence 1, Appl
45	126	2.7	10254	4	US 08 961 527 29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-204-429-2
Sequence 2, Application US/08204329
Patent No. 5710255
GENERAL INFORMATION:
APPLICANT: SHEPARD, H. M.
APPLICANT: WEN, SHU F.
TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI FLUOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND & TOWNSEND, 5 CROWN LIP
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/204, 429
FILING DATE: 15 AUG 1994
CLASSIFICATION: 4.0
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05866
FILING DATE: 14-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: RENE A. KILIS
REGISTRATION NUMBER: 45,146
REFERENCE/SECRET NUMBER: 16440 00040005
TELEPHONE: (415) 426 2400
TELEFAX: (415) 426 2422

479 GTTTCATCTGAGATGAGTAATGGAGGTTATATTCAAAAGAAAAAGAAAGTGTGGGGA 438
 77 ValAspLeuAspGluMetSerPheThrPheThrGluLeu 89
 499 ATCTGTATCTTATATGAGTATGAGCTAGATGAGATGGCTGCTACATTTTACTGAGCTA 498
 90 GluLysAsnIleThrLeuSerValHisLysPhePheAsuLeuLeuLysGluIleAspThr 109
 499 CAGAAAAACAATAGAAATCAGTGGTAAATAAAATCTTAACTTACTTAAAGAAATGATACC 558
 110 SerThrLysValAspAsuAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAla 129
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 140 LeuPheSerLysLeuGluArgIleCysGluLeuIleTyrLeuThrGluProSerSerSer 149
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 160 IleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu 169
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 190 CysValIleAspTyrPheIleLysLeuSerProPheMetLeuLeuLysGluProTyrLys 209
 799 TCTTCTTCTGATTTATTTATTAATCTCTACCTGCTGATGTTGCTCAAAAGACATATAA 858
 210 ThrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGluAsnArgSer 229
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 240 AlaArgIleAlaLysGluLeuGluAsnAspThrArgIleIleGluValLeuCysLysGlu 249
 919 GATGGATAGCAAAATGAGAAATGATACAAAGATTTATGAGTTCTCTGTAAGAA 978
 250 HisCysLysAsnIleAspGluValLysAsuValTyrPheLysAsnIleThrPheMet 269
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 290 TyrGluGluIleTyrLeuLysAsuLysAspLeuAspAlaArgLeuPheLeuAspHisAsp 309
 1099 TACGAAATAATTAATTAATAATTAATGATGATGATGATGATGATGATGATGATGATG 1158
 310 LysThrLeuGluThrAspSerIleAspSerPheGluThrGluArgThrProArgLysSer 329
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 570 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThrThr 589
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 590 ArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAlaPheGluThrGluLys 609
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 2419 ATGCACAGACATCAAAATCAAAATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2478
 750 ProfileProHisIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 769
 2479 CCAATACCT 2538
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740 ThrThrLysMetThrProAspSerArgIleLeuValSerIleuLysLysAspPheGly 839
 750 AATCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 2658
 760 ThrSerGluLysPheGluLysIleAspGluMetValCysAsnSerAspArgValLeuLys 829
 770 ACTTCGAGAAATTCGAGAAATTCGAGAAATTCGAGAAATTCGAGAAATTCGAGAA 2718
 780 ArgSerAlaGluGlySerAsnProProLysProLysLysLysLeuArgPheAspIleGlu 849
 790 AGAAGTGTCTGAAG 2778
 800 GlySerAspGluAlaAspGlySerLysIleLeuProGlyGluSerLysPheGlnLys 869
 810 GCAACATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2838
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 830 CTGAGCAAAAT 2898
 840 AspThrSerAsnLysGluGluLys 897
 850 GATACCTGACAAAG 2922

RESULTS

PCT-US94-10357-1

Sequence 1: Application: PCT/US94/10357

GENERAL INFORMATION:

APPLICANT: The Regents of the University of California
 APPLICANT: and Camille, Inc.
 TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma
 GENE
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive
 CITY: San Diego
 STATE: California
 COUNTRY: USA

ZIP: 92122

COMMUNICABLE FORM:

C-METER: IBM PC compatible

C-METER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/10357

FILING DATE: 13-SEP-1994

CLASSIFICATION:

PCT APPLICATION DATA:

APPLICATION NUMBER: US 09/121,108

FILING DATE: 13-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 41,815

REFERENCE CHECKED NUMBER: 40-007 1117

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 2994 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

POLYMER: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 139...2923

PCT-US94-10357-1

Alignment Scores:

Pred. No.: 0

Length: 2994

Score: 4602.50 Matches: 896
 Percent Similarity: 96.66% Conservative: 1
 Best Local Similarity: 96.55% Mismatches: 0
 Query Match: 94.38% Indels: 31
 DB: 5 Gaps: 1

US-09-026-459a-41 (1-897) x PCT-US94-10357-1 (1-2994)

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 QY 21 ProAlaProProProProProProProProProProProProProProPro 40
 DB 199 CCGGACCG 258
 QY 41 AspleuProLeuValArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeu 60
 DB 259 GAGTGTCT 318
 QY 61 CysGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 76
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 QY 77 ----- ValAspLeuAspGluMetSerPheThrPheThrGluLeu 89
 DB 439 ATCTGTATCTTTTATTTGAGAGATTTATTTATTTATTTATTTATTTATTTAT 498
 QY 90 GlutLysAsnLysGluLysValHisLysPhePheAsnLysLysLysLysLysLys 109
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 DB 919 GATGGATACCAAAACATAGAAAAATGATAGAAATTAATGAAAGTCTCTGTAAG 978
 QY 250 HisGlnCysAsnLysCysGluValLysAspValLysPheLysAspPheThrPhePhe 269
 DB 979 CATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAATTTATATCT 1038
 QY 270 AsnGluLeuGlyLysValThrSerAspGlyLysPheGluValGluAsnLysLysAsp 289
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Db      2839  CTGGGACAGAAATCACTTCTATCTCCAACTCAATATCAAAAATCAAAAATCAAAAATCAAAAATCAATG 2898
QY      890  AspThrSerAsnLysGluGluLys 897
Db      2899  GATACCTCAAAACAAGAGAGACAA 2922
RESULT 8
US-08 038 760-1
: Sequence 1, Application US/08048760
: Patent No. 5496741
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong Ji
: APPLICANT: Hu, Shi Xue
: APPLICANT: Benedict, William F.
: TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
: TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/048,760
: FILING DATE: 19980325
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Polissant, Brian M
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCCKET NUMBER: 7409-025-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 740-9090
: TELEFAX: (212) 869-9741/8964
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4232 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 19...2469
US-08-038-760-1

Alignment Scores:
Pred. No.: 0 Length: 4232
Score: 4218.00 Mismatches: 620
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 90.97% Indels: 0
Dh: 1 Gaps: 0

US-09-026-459A-41 (1-897) x US-08-038 760-1 (1-4242)

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QY 98 HisLysPhePheAsnLeuLeuLysGluTrpAspThrLysValAsnAlaMet 117

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478 ThrAspLeuSerPheProTrrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPhe 497
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499 TAAATATGATGAGAAAGTTTATTCAAGATAGAAAGCAATTCACAAAGAGAAATGATATA 1911
518 HistLeuGluArgCysGluHisArgIleMetGluSerLeuAlaIlePheLeuSerAspSerPro 537
519 ZATTAGACAGATGTAACAAATCAAAATCAATGAAATGAAATGAAATGAAATGAAATGAA 1851
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558 ThrValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla 597
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619 GTTTTATTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1551
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639 CT 1491
658 GluAsnGluThrGluLeuMetArgAspArgHisLeuAspGluIleMetLysSerMet 677
659 CAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1431
678 LysGlyIleCysLysValLysAsnIleCaspLeuLysPheLysIleIleValThrAlaThr 697
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698 LysAspLeuProHisAlaValGluGluThrPheLysArgValLeuIleLysGluGlu 717
699 AAGCACTTCT 1311
718 TyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnIle 737
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738 LeuGlnIleAlaSerThrArgProThrLeuSerProIleProHisIleProArgSer 757
739 TTTCAATATCT 1191
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759 CTATTAAGTTTCT 1131
778 LeuLysSerProTyrLysIleSerGluGlyLeuPheProThrProThrLysMetThrProArg 797
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799 TAAAGATCTTAT 1011
818 AsnIleMetValCysAsnSerAspArgValLeuLysArgSerAlaGluCysAsnPro 837
819 AAT 951
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959 AAT 831
878 ThrArgMetGlnLysGlnLysMetAsnAspSerMetAspThrSerAsnLysGluGluLys 897
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RESULT 10
US-08-470-091-1
Sequence 1, Application US/08470091
Patent No. 5913236
GENERAL INFORMATION:
APPLICANT: Xu, Hong Ji
APPLICANT: Hu, Shi-Xue
APPLICANT: Benedict, William F.
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
METHOD OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
NUMBER OF SHOWNCHS: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,091
FILING DATE: JUN-16-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/038,760
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,462
PRACTICE/PHONE NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3242 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19..2469
US-08-470-091-1
Alignment Scores:
pred. No.: 0 Length: 3232
Score: 4213.00 Matches: 820
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.97% Indels: 0
DB: 2 Gaps: 0
US-08-026-459a-41 (1-897) x US-08-470-091-1 (1-3232)
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7 CACTTAAATGATGATGCTTACCTTTTACGAGCTACAGAAAAACATGACATGCTG 66
 98 HSLysPhePheAsnLeuLeuLysGluLeuAspThrSerThrLysValAspAsnAlaMet 117
 117 TGGGCTCTTGAGGTGGTAATGGCCACATATAGACAAAGCATATTTAGAAATCTGATCT 1206
 67 CATAAATCTTAACTTAACTAAAGAAATGATACAGTACCAAGAACTTGATAATGCTATG 126
 116 SerAspLeuLeuLysGlyTyrAspValLeuPheAlaLeuPheSerLysGluGluArgThr 147
 127 TCAAGATCTTTGAAATGAAATATGATGATGATTTTGGCACTCTTCAGCAAAATTTGAAAGACA 186
 148 CysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 157
 167 TGGAGCAATTAATATATGACACCAACAGCAGCTTCGATATCTACAGAAATAAAATCTGCA 246
 168 LeuValLeuLysValSerTrpIleThrPheLeuLeuAlaLysGlyGluValLeuGluMet 177
 247 TTGGTGGTAAAGATTTCTGATGATGATTTTATATGATGATGATGATGATGATGATGATG 306
 178 GluAspAspGluValIleSerPheGluLeuMetLeuCysValLeuAspTyrPheIleLys 197
 407 GAAGATGATCTGGGATTTTCACTTAAAGTATGATGATGATGATGATGATGATGATGATGAT 366
 198 LeuSerProMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsnGly 217
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 218 SerProArgThrProArgArgGlyGluAsnArgSerAlaArgIleAlaLysGluLeuGlu 237
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 248 AsnAspThrArgIleGluValLeuCysLysGluLeuLeuLeuLeuLeuLeuLeuLeuLeu 257
 487 AATGATACAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 546
 258 LysAsnValTyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSer 277
 547 AAAAAAGTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
 278 AsnGlyLeuProGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 297
 607 AATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
 298 LysAspLeuAspAlaArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 317
 667 AATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
 318 AspSerPheGluThrGluArgThrProArgLysSerAsnLeuAspGluGluValAsnVal 337
 727 CAAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
 338 IleProProIleThrProValArgThrValMetAsnThrIleGluLeuLeuMetMetIle 357
 787 ATTCGTCACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846
 358 LeuAsnSerAlaSerAspLeuProSerGluAsnLeuLeuSerTyrPheAsnAsnCysThr 377
 847 TTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906
 378 ValAspProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLysGlu 397
 907 GTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
 398 LysPheAlaLysAlaValGlyGlyCysValGluLeuLeuLeuLeuLeuLeuLeuLeuLeu 417
 967 AATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
 418 GlyValArgLeuTyrTyrArgValMetGluSerMetLeuLysSerGluGluArgLeu 437
 1027 GCAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1086
 438 SerIleGluAsnProSerLysLeuLeuAspAsnIlePheIleMetSerLeuLeuLeuAla 457
 1087 TCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1146

458 CysAlaLeuGluValIleMetAlaThrTyrSerArgSerThrSerGluAsnLeuAspSer 477
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 478 GlyThrAspLeuSerPheProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPhe 497
 1207 GCAACACAGATTTGCTTTGCTATGCAATGCTGAAATGCTGAAATGCTGAAATGCTGAAAT 1266
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 518 HisLeuGluArgCysGluHisSerGluMetGluSerLeuAlaIlePheSerAspSerPro 537
 1327 CATTTAAGCATGTGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1486
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 1627 CAGTTTATAAAAAGTCTATGCTGCTAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1686
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 718 TyrAspSerIleIleValPheTyrAsnSerValPheMetGluAlaGluLysThrAsnIle 737
 1927 TATGATCTTATAGATCTTATAGATCTTATAGATCTTATAGATCTTATAGATCTTATAG 1986
 738 LeuGluThrAlaSerThrArgProProThrLeuSerProIleProIleHisLeuProArgSer 757
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 758 ProTyrLysPheProSerProLeuArgIleProGlyLysValLysIleLysIleLysIle 777
 2047 CTTTCAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2106
 778 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg 797
 2107 GCGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2166
 798 SerArgIleLeuValSerIleGlyLysSerIleGlyLysThrSerGluLysPheIleLysIle 817
 2167 TCAAGAACTCTACTATCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2226

[illegible]

RESULTS 1:
 US 08 476 051-2/c
 : Seq. class 2. Application US 08476051
 : Patent No. 5912236
 : GENERAL INFORMATION:
 : APPLICANT: XU, Hong-ji
 : APPLICANT: HO, Shi-xue
 : APPLICANT: Benedict, William F.
 : TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products
 : TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.

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1010 TCAAGAACTTATAGTATCAATGGTGAATCATTCGGAAATCTTCAGAGAGTCTCAAAAAA 1011
1011
1012 AsnGlnMetValCysAsnSerAspAlaValLeuLysArgSerAlaLeuLysSerAspPro 847
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1024 ThrArgMetGlnLysGlnLysMetAspAspSerMetAspThrSerAsnLysLeuLys 897
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RESULT 12
US-08-842-883-1
: Sequence 1, Application US/08842883
: Patent No. 5807681
: GENERAL INFORMATION:
: APPLICANT: Giordano, Antonio
: APPLICANT: Baldi, Alfonso
: TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
: NUMBER OF SEQUENCES: 115
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SEIDEL, GONIA, LAVAGNA & MINATO, P.O.
: STREET: Suite 1800 Two Penn Center Plaza
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19102
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.40
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/842,883
: FILING DATE:
: CLASSIFICATION: 4.5
: ATTORNEY/AGENT INFORMATION:
: NAME: Monaco, Daniel A
: REGISTRATION NUMBER: 30,480
: REFERENCE/POWER NUMBER: 8421-14 US1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-8383
: TELEFAX: (215) 568-5549
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4854 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 70..3489
: US-08-842-883-1

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Alignment Scores: 4.1e 71 Length: 4854
 Pred. No.: 813.50 Matches: 287
 Score: 37.71% Conserved: 176
 Best Local Similarity: 24.68% Mismatch: 452
 Query Match: 17.57% Indels: 403
 DB: 1 Gaps: 49

US-09-026-459A 41 (1 897) x US-08-842-883-1 (1 4854)


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16 2161 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
17 590 ArgValAsnSer ..... ThrAla 595
16 2221 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
17 596 Asn ..... 596
16 2281 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
17 597 ..... AlaGlnThrGlnAla ..... ThrSerAlaPhe 605
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17 606 Gln ..... 606
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16 2461 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
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16 2521 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
17 618 LeuPheThrLeuValAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAla 637
16 2581 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640
17 638 Leu LeuSerGlnHisProGlnLeuGlnHisThr 656
16 2641 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2694
17 657 LeuGlnAsnGlnLeuGlnLeuMetArgPheSerLeuAspGlnLeuMetCysSer 676
16 2695 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2754
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16 2755 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2814
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16 3055 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3114
17 732 ArgLeuLeuThrAsnThrLeuGlnThrAlaSerThrArgProProThrLeuSer 749
16 3115 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3174
17 750 ProLeuProGlnHisLeuProArgSerProLeuGlySerProLeuGlySerProLeuGlySerProLeu 768
16 3175 AATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3216

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17 769 ..... ProGlyGlyAsnLeuThrLeuSerProLeuGlySerProLeuGlySerProLeuGlySer 786
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17 787 GlyLeuProThrProThrLeuMetThrProAlaSerArgGlnLeuValThrLeuGlyGln 806
16 3279 ..... GAAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3338
17 807 SerProThrThrSerGlnPheLeuGlySerProLeuGlySerProLeuGlySerProLeuGlySer 824
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17 827 ValLeuLeuArgSerAlaLeuGlySerAsnProProLeuGlySerProLeuGlySerProLeuGlySer 846
16 3399 ..... CCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3458
17 847 AspLeuGlnGlySerAspGlnAlaAspGlySerThrLeuGlySerProLeuGlySerProLeuGlySer 865
16 3459 ..... CTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3518
17 866 PheGlnGlnLeuAlaLeuMetThrSerThrArg 877
16 3519 ..... TATTACGGCTGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3578
17 877 ..... 877

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RESULT 13

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US-08-832-877-1
Sequence 1, Application US/08842877
Patent No. 5840506
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, GUNDA, LAVORGNA & MANNO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 446
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8421 14 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8483
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4853 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 70..489
US-08-832-877-1

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Alignment Scores:
Pred. No.: 4,16 71
Score: 814.50
Percent Similarity: 47.71%
Length: 4853
Matches: 287
Conservative: 176

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1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes the need for transparency and accountability in financial reporting.

2. The second part of the document outlines the various methods and techniques used to collect and analyze data. It includes a detailed description of the experimental procedures and the statistical analysis performed.

3. The third part of the document presents the results of the study, showing the trends and patterns observed in the data. It includes several tables and figures to illustrate the findings.

4. The fourth part of the document discusses the implications of the results and provides recommendations for future research. It highlights the areas that need further investigation and the potential applications of the findings.

5. The fifth part of the document is a conclusion, summarizing the main points of the study and the overall findings. It reiterates the importance of the research and the need for continued efforts in this field.

DB 2166 ATGAGAAATGATATGATGAAATGATGAGATGAGGAGATGTCAGAAATTCGAAATAT 2225
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DB 2286 TATTAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2345
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QY 2757 TATTAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2816
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QY 3417 TATTAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3461
DB 3186 TATTAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3240

RESULT 2

US-08-048-760-2/c
Sequence 2, Application US/08048760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Hu, Shi-Xue
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
METHODS FOR Tumor Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatentLib Release #1.0, Version #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/048,760
FILING DATE: 1998-04-25
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOC# NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4242 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
US-08-048-760-2

Query Match 94.1% Score 4224.4 DB 1: Length 4242
Best Local Similarity 100.0% Pred. No. 0
Matches 4224: Conservatve 0, Mismatches 1, Gaps 0
QY 237 CGAGCTAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 206
DB 3231 CGAGCTAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4172
QY 247 CGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 406
DB 3171 CGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4112
QY 357 GTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 416
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QY 417 ATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 476
DB 3051 ATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2092
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DB 2991 ATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2942
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DB 1038 AGAAGATTTTGAACAACAGAGAACACGAGAAAAGTAACCTTGTGATGAAGAGGTGAATGT 785
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DB 1054 GGGAGTTCAGCTTGTGATACCGAGTAAATGGAATCCATGCTTAAATCAGAGAGAACGAT 1265
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DB 1058 ACATTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1385
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DB 1064 TTTAAATCAGCAGAGCTGACAACTTTCAGAAAATCAGATTTCTTATTTTAAACACTGAC 1565
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QY 1067 ACTTTTATTAATAAATAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1916
DB 1068 ACTTTTATTAATAAATAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1685
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DB 2586 TTTAAATCAGCAGAGCTGACAACTTTCAGAAAATCAGATTTCTTATTTTAAACACTGAC 2645
QY 2877 GTATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2936
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DB 2706 TTTAAATCAGCAGAGCTGACAACTTTCAGAAAATCAGATTTCTTATTTTAAACACTGAC 2765
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[illegible][illegible]

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 55323400

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3249 base pairs

TYPE: nucleic acid

STRANDEDNESS: Single

TOPOLOGY: Linear

FEATURES:

US 08 429-264-1

Query Match: 2.98; Score 68.2; DB 1; Length 3249;

Best Local Similarity: 53.08; Pctd. No. 1 7e-07;

Matches 170; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

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QY 1889 ATCTGCGCTAAATATACATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1948

DB 2432 CTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2428

QY 1949 TCACTGAGAGGCTTTTCCAGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2008

DB 2429 AAATCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2488

QY 2009 ATTTGACCAAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2068

DB 2489 ATTTGACCAAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2548

QY 2069 TTAATTTAAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2128

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QY 2129 TCAAGCTTTTGTATCAAG 2149

DB 2609 ATAGAGCTTTTGTATCAAG 2629

RESULTS:

US 08 812 883-1

Sequence 1, Application US/08812883

Patent No. 5807681

GENERAL INFORMATION:

APPLICANT: Baldi, Alphonso

TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS

TITLE OF INVENTION: OF CANCER

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEIDEL, GUNDA, LAVORNA & MONACO, P.C.

STREET: Suite 1800 Two Penn Center Plaza

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patchin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/812,883

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 8321-13 US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4853 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: Linear

MOLECULE TYPE: cDNA

FEATURES:

NAME/KEY: CDS

LOCATION: 70..3489

US-08-832-883-1

Query Match

2.09; Score 68.2; DB 1; Length 4853;

Best Local Similarity

53.68; Pctd. No. 2.1e-07;

Matches 170; Conservative

0; Mismatches 148; Indels

3; Gaps

1;

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DB 2729 ATTTGACCAAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2788

QY 2069 TTAATTTAAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2128

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QY 2129 TCAAGCTTTTGTATCAAG 2149

DB 2849 ATAGAGCTTTTGTATCAAG 2869

Search completed: January 17, 2003, 18:23:20

Job time : 111.021 secs


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156  1030  CTTTATCAAAATTCCTGGACCTTCGTAACATCAATGGACTCCACAGGTTCAAAATCTT 1089
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170  282  ValMetAsnThrIleGlnGlnIleLeuMetIleLeuAsnSerAlaSerAspGlnProSer 301
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199  |||||
200  1690  CTAAATGCTGCTTAATTTAAAGAGCTTGATTTTACAAAGTGAAGAAATTTTATCAAA 1749
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206  462  MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLys 481
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208  1810  ATGAAATGCTTGCATGCTGCTCAGATTCACCTTTATTATTGATCTATTATAACAATCAAG 1869
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RESULT 3

AA041545

ID AA041545 standard; DNA; 2994 bp.

XX

AC AA041545;

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FF /product= "pLacZneo"
 FF /note= "retinoblastoma tumour suppressor"

XX RS09-026-459a-35

FF 34 AAT 1999

XX 28 001-1997 970S 0959648

XX 25 001-1994 940S-0428673

XX 25 001-1994 940S-0428669

FF MAY 1994 940S-0428606

XX 24 001-1997 940S-0428648

XX (CAN-1) CAN-1 INC

FF Gen 13 97 Maximal 97 Willk 97

XX W01 1999-443568/47

XX 1-0016 AAY2471

XX Genbank adenoviral vectors useful for gene therapy of cancer,

XX especially p53 deficient tumours

XX (also, see: Fig 3; 50pp; English)

XX The present invention describes a composition comprising a recombinant

XX adenovirus expression vector, where the vector has an insert of

XX exogenous DNA comprising a gene encoding a foreign protein and

XX adenovirus DNA in which all of the coding sequences of E1a, E1b, and

XX protein IX, and part of E3 are deleted. The vectors are useful in gene

XX therapy treatment of cancer, especially for treating p53 deficient

XX tumours. The vector encodes safer and more efficient gene therapy of

XX cancer. The present sequence encodes human p10-RB retinoblastoma

XX tumour suppressor which can be used as the foreign gene in the above

XX vector.

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FF /product= "pLacZneo"
 FF /note= "retinoblastoma tumour suppressor"

XX RS09-026-459a-35

FF 34 AAT 1999

XX 28 001-1997 970S 0959648

XX 25 001-1994 940S-0428673

XX 25 001-1994 940S-0428669

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XX cancer. The present sequence encodes human p10-RB retinoblastoma

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XX vector.

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FF /product= "pLacZneo"
 FF /note= "retinoblastoma tumour suppressor"

XX RS09-026-459a-35

FF 34 AAT 1999

XX 28 001-1997 970S 0959648

XX 25 001-1994 940S-0428673

XX 25 001-1994 940S-0428669

FF MAY 1994 940S-0428606

XX 24 001-1997 940S-0428648

XX (CAN-1) CAN-1 INC

FF Gen 13 97 Maximal 97 Willk 97

XX W01 1999-443568/47

XX 1-0016 AAY2471

XX Genbank adenoviral vectors useful for gene therapy of cancer,

XX especially p53 deficient tumours

XX (also, see: Fig 3; 50pp; English)

XX The present invention describes a composition comprising a recombinant

XX adenovirus expression vector, where the vector has an insert of

XX exogenous DNA comprising a gene encoding a foreign protein and

XX adenovirus DNA in which all of the coding sequences of E1a, E1b, and

XX protein IX, and part of E3 are deleted. The vectors are useful in gene

XX therapy treatment of cancer, especially for treating p53 deficient

XX tumours. The vector encodes safer and more efficient gene therapy of

XX cancer. The present sequence encodes human p10-RB retinoblastoma

XX tumour suppressor which can be used as the foreign gene in the above

XX vector.

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PS E PSDB: AAE00689

XX New recombinant adenovirus expression vector having a gene encoding for
 P1 a foreign protein and a partial or total deletion of the adenoviral
 P1 protein IX DNA, useful in gene therapy for treating or reducing

XX hyperproliferative cells

PS Disclosure: Fig 3; 4pp; English.

XX The present cDNA sequence encodes retinoblastoma (Rb) tumour suppressor
 protein, designated as p10RB.

XX the invention relates to a recombinant adenovirus expression vector
 characterized by the partial or total deletion of the adenoviral protein
 IX DNA beginning at nucleotides 357 or 360 and ending at 4020 4050, and
 having a gene encoding a foreign protein such as tumor suppressor

XX protein, p10RB (retinoblastoma) and p53. Adenovirus vector is used
 for screening tumor suppressor genes useful in gene therapy. The vector

XX is particularly useful for treating or reducing hyperproliferative cell
 disorders such as thyroid hyperplasia, Grave's disease, psoriasis,

XX benign prostatic hypertrophy, Li-Fraumeni syndrome, cancers specifically
 hepatocellular carcinoma, neoplasms, leukemias, lymphomas, etc. to

XX inhibit tumour proliferation or to ameliorate particular related
 pathology such as sickle cell anaemia and Tay-Sachs disease. The vector

XX is also useful for the safe recombinant production of diagnostic and
 therapeutic polypeptides and proteins.

XX Sequence: 2995 RP: 975 A: 618 C: 593 G: 809 T: 0 other:

Alignment Scores:

Prod. No.: 0 Length: 2995
 Score: 4274.00 Matches: 841
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.88% Indels: 0
 Dbs: 22 Gaps: 0

95 09 026 459a 35 (1 832) x AA:04474 (1-2995)

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DB 40 CTGCGGAGAACTCTGATCTTATGACAGCAGTGGCTGATAGATGAGATGGTGTCACCTTT 489

QY 22 ThrThrLeuGlnIleGlySerValHisIlePheAsnLeuLeuLysGlu 41

DB 490 ACTGAGCTACAGAAANATACAAATGCTGCTCATAAATCTTACTTAAAGAA 549

QY 42 IleAspThrSerThrLysValAspAlaMetSerArgLeuLeuLysTyrAspVal 61

DB 550 AATGATAATAGTAATGATAATGATAATGATAATGATAATGATAATGATAATGATA 609

QY 62 LeuPheAlaLeuPheSerLysLeuAlaThrCysIleLeuIleTyrLeuThrGluPro 81

DB 610 TGTGTGATCT 659

QY 82 SerSerSerIleSerThrThrIleAsnSerAlaLeuValIleLysValSerThrPheThr 101

DB 670 AGCAATCTGATATCTATGAAATTAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 729

QY 102 PheLeuLeuAlaLysGlyGlyValLeuGluMetGluAspAspLeuValIleSerPheGlu 121

DB 740 TTTTATATATGCTAAAGGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 789

QY 122 LeuMetLeuLysValLeuAspTyrPheIleLysLeuSerProMetLeuLeuLysGlu 141

DB 790 TTAATGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849

QY 142 ProLysThrAlaValIleProIleAsnGlySerProArgThrProArgGlyGlu 161

DB 850 GATATAAATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909

QY 162 AsnArgSerAlaAlaIleValLysGluLeuGluAsnAspThrArgIleLeuValLeu 181

DB 910 AACAGGAGTGGAGGATAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 959

QY 182 CysLysSerHisGluCysAsnIleAspIleValLysAsnValIlePheLysAspMetIle 201

DB 970 TGTAAANANATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1029

QY 202 ProMetAsnSerLeuGlyLeuValIleSerAsnGlyLeuProIleValIleAsnGlu 221

DB 1030 CTTTTATCAATCTCTGGACCTTGAACATCTAAAGCATCTGATGATGATGATGATGATGATGAT 1089

QY 222 SerLysArgTyrGlyGlyIleTyrIleAsnAspMetIleAspAlaLeuPheVal 241

DB 1090 TCTAAACATACGAGAGAAATTAATTAATAAATAAAGATCTAGATGTAAGATTAATTAATTAAT 1149

QY 242 AspHisAspLysThrLeuGlnIleAspSerIleAspSerIleAspSerIleAspSerIleAsp 261

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QY 262 ArgLysSerAsnLeuAspGluValAsnValIleProProHisThrProValArgThr 281

DB 1210 CCAAAAGTAACCTTGAAGACAGTCAATCTAAATCTGATGATGATGATGATGATGATGATGAT 1269

QY 282 ValMetAsnThrIleGlnIleLeuMetMetIleLeuAsnSerAlaSerAspIleProSer 301

DB 1270 GTTGAACACATCTCAACAACTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1329

QY 302 GluAsnLeuIleSerTyrPheAsnAsnGlyThrValAsnProLysIleSerIleLeuLys 321

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DB 1750 GCAAGAAAGCACTTCAAG 1809

QY 462 MetGluSerLeuAlaIlePheSerAspSerPheLeuPheAspLeuIleLysIleSerLys 481

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DB 1870 GACGAG 1929

QY 502 AsnAsnHisThrAlaIleAspMetTyrLeuSerProValIleArgSerProLysLysLysGly 521

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QY 522 SerThrThrArgValAsnSerThrAlaAsnAlaGluThrIleAlaThrSerAlaPheGlu 541

DB 1990 TCAACTAGCGCTGTAATCTTACTGCAAAATGACACACAAATGACAAATGACAAATGACAAATGACAA 2049

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 610 TGGTTGATCTCTCAACAAATGGAAAGAACAGGACGATATATATATATATATAT 669
 82 SerSerSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 101
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PR 20-FEB-1997; 970S-0038755.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX Hu S, Loquethis CJ, Xu H, Zhou Y;
XX WPI; 1998-480796/41.
XX P-PSDB; AAW71354.
XX
XX New tetracycline responsive expression vectors - used for the
XX tightly controlled expression of genes, such as tumour suppressor
XX genes for treating cancers
XX
XX Disclosure: Pages 145-150; 190pp; English.
XX
XX The present sequence appears in the specification, which describes a
XX tetracycline responsive expression vector (TREV), which contains a
XX sequence encoding a fusion protein comprising a transcriptional
XX transactivation domain (TAD) operatively attached to a tetracycline
XX repressor protein (TRP), the first sequence operatively positioned
XX downstream of a promoter. The vector also contains a cloning site
XX operatively positioned downstream of a basal promoter comprising a
XX tetracycline operator. The TREVs can be used to produce stable cell
XX lines in which gene expression is tightly regulated by tetracycline.
XX They can be used for the production of proteins such as tumour
XX suppressor proteins which can be used for treating diseases characterised
XX by abnormal cellular proliferation, particularly cancers.
XX
XX Sequence 3555 BP; 1171 A; 584 C; 653 G; 1047 T; 0 other;
XX

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Best Local Similarity: 100.00% Indels: 0
Query Match: 99.88% Gaps: 0
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QY 162 AsnArgSerArgGlyGlyAlaGlyGlnLeuGluAsnAspThrArgIleIleGlnValLeu 181

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1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

2. The second part of the document is a list of the topics that were discussed at the meeting. The topics are listed in alphabetical order.

3. The third part of the document is a list of the actions that were taken at the meeting. The actions are listed in alphabetical order.

4. The fourth part of the document is a list of the decisions that were made at the meeting. The decisions are listed in alphabetical order.

5. The fifth part of the document is a list of the recommendations that were made at the meeting. The recommendations are listed in alphabetical order.

Best local similarity 100.0%; Pred. No. 0;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23 10 TGTGGGAAATCTGATGCTTATTTGAGACAGTGGAGUAGATGAGATGGTTCACATTTT 69
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Db 187 AATGAGCAGACAAACAAACAGTGGAGATGAGATGGTTCACATTTT 246
QY 190 TGTGGGAAATCTGATGCTTATTTGAGACAGTGGAGATGAGATGGTTCACATTTT 249
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FIGURE 12

AA004501
 ID: AA004501 Standard: cDNA; 4597 bp.

XX AA004501;

XX 05 JUL 1999 (first entry)

DE Human retinoblastoma gene cDNA.

KW Retinoblastoma; Rb gene; human; predisposition; diagnosis; therapy;

KW ss.

XX Homo sapiens.

XX Key location/qualifiers

FF 005 357...2797

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 1552 AATAAATGCTTTCAGAGGCTCTCAATATCACCTTTATTTGATCTTTATTAACAATCAAAAG 2637
 1553 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2638
 1554 GATATGCTTTCAGAGGCTCTCAATATCACCTTTATTTGATCTTTATTAACAATCAAAAG 2409
 1555 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2410
 1556 AATAAATGCTTTCAGAGGCTCTCAATATCACCTTTATTTGATCTTTATTAACAATCAAAAG 2697
 1557 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2698
 1558 GATATGCTTTCAGAGGCTCTCAATATCACCTTTATTTGATCTTTATTAACAATCAAAAG 2469
 1559 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2470
 1560 AATAAATGCTTTCAGAGGCTCTCAATATCACCTTTATTTGATCTTTATTAACAATCAAAAG 2757
 1561 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2758

2470 GATATGCTTTCAGAGGCTCTCAATATCACCTTTATTTGATCTTTATTAACAATCAAAAG 2529
 2471 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2530
 2472 AATAAATGCTTTCAGAGGCTCTCAATATCACCTTTATTTGATCTTTATTAACAATCAAAAG 2817
 2473 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2818
 2474 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 2589
 2475 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2590
 2476 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 2877
 2477 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2878
 2478 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 2649
 2479 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2650
 2480 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 2837
 2481 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2838
 2482 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 2937
 2483 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2938
 2484 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 2769
 2485 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2770
 2486 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3057
 2487 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3058
 2488 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 2829
 2489 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2830
 2490 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3117
 2491 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3118
 2492 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 2889
 2493 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2890
 2494 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3177
 2495 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3178
 2496 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 2949
 2497 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2950
 2498 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3237
 2499 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3238
 2500 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3009
 2501 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3010
 2502 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3297
 2503 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3298
 2504 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3069
 2505 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3070
 2506 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3357
 2507 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3358
 2508 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3129
 2509 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3130
 2510 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3417
 2511 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3418
 2512 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3189
 2513 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3190
 2514 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3477
 2515 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3478
 2516 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3249
 2517 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3250
 2518 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3437
 2519 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3438
 2520 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3266
 2521 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3267
 2522 TGTCTATACCTCTGCAATTTATTTGATCTTTATTTGATCTTTATTTGATCTTTATTTGATCTTT 3554
 2523 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 3555

RESULT 14

AAV58446

ID AAV58446 standard; DNA: 3323 BP.

XX AAV58446;

XX 02-DRC-1998 (first entry)

XX Modified retinoblastoma tumour suppressor gene.

 XX Modified retinoblastoma tumour suppressor; RBP protein; cancer therapy;
 XX cellular proliferation inhibitor; ss.
 XX Homo sapiens.

 Key Location/Qualifiers
 Key


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XX W098-0091-A2.
XX 27 APR-1998.
XX
XX 19-FEB-1998; 98W0-US03041.
XX
XX 20-FEB-1997; 97US-0038118.
XX
XX (BAYLOR) BAYLOR COLLEGE MEDICINE.
XX (TEXAS) UNIV TEXAS SYSTEM.
XX
XX Benedict WF, Hu S, Xu H. Zhou Y.
XX
XX W098-0098-41.
XX PFSUB: AAW69367.
XX
XX Refinoblastoma suppressor protein with N-terminal modification -
XX inhibiting cellular proliferation, particularly cancer
XX
XX Claim 22: Page 158 L62, 349FP, English.
XX
XX This sequence encodes a modified refinoblastoma tumor suppressor
XX protein (RTSP) of the invention. The proteins can be used for inhibiting
XX cellular proliferation when coadministered with a p53 protein. The p53ps
XX can be used for treating diseases characterized by abnormal cellular
XX proliferation, particularly cancers. The RTSPs have a broader spectrum of
XX activity than wild type RTSPs.
XX
XX Sequence 3323 BP: 1114 A: 605 C: 591 G: 1013 T: 0 other;
XX
XX Alignment Scores:
XX
XX Pred. No Length 3323
XX Score: 4372.00 Matches: 851
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Matches: 100.00% Indels: 0
XX DB: 19 Gaps: 0
XX
XX us-09-026-459a-33 (1-851) x AAW58443 (1-3323)
XX
XX 1 MetGluLysValSerSerValAspGluValLeuGlyClyTyrIleClnLysLysGlu 20
XX
XX 7 ALGACAAAGTTCATGCGGAGTGTGAGTATGCGGAGTATATATCAAGAGAAAGGAA 66
XX
XX 21 LeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspGluMetSerPheThrPhe 40
XX
XX 67 ATGAGGAAATCTGATATCTTATGCGGAGTGTGAGTATATATCAAGAGTATATCTT 126
XX
XX 41 ThrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeuLysGlu 60
XX
XX 127 AGTGAAGTACAGAAATATAGAAATATGTCGATATATATCTTAACTTACTTAAAGAA 186
XX
XX 61 IleAspThrSerThrLysValAspAsnAlaMetSerArgLeuLysLysLysValAspVal 80
XX
XX 187 ALGACAAAGTTCATGCGGAGTGTGAGTATGCGGAGTATATATCAAGAGTATATCTT 246
XX
XX 81 LeuPheAlaLeuPheSerLysIleLeuArgThrCysGluLeuIleTyrLeuThrGlnPro 100
XX
XX 249 TGTGTCACATCTGCGGAGTGTGAGTATGCGGAGTATATATCAAGAGTATATCTT 306
XX
XX 101 SerSerSerThrGluIleAsnSerAlaIleValLeuLysValSerTrpIleThr 120
XX
XX 107 AGTGAAGTACAGAAATATAGAAATATGTCGATATATATCTTAACTTACTTAAAG 366
XX
XX 121 PheLeuLeuAlaLysGlyGluValIleGlnMetGluAspAspLeuValIleSerPheGln 140
XX
XX 167 TTTTATATGCGGAGTGTGAGTATGCGGAGTATATATCAAGAGTATATCTTAAAG 426
XX
XX 141 LeuMetLeuLysValLeuAspTyrPheIleLysLeuSerProMetLeuLysGlu 160
XX
XX 427 TTAATGCTATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 486

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QY 161 ProTyrTrpThrAlaValIleLeuValIleLeuValIleLeuValIleLeuValIleLeu 180
DB
DB 487 GCAATATATATATATATATATATATATATATATATATATATATATATATATATATAT 546
QY 181 AsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeu 200
DB
DB 547 AACAGGATTCACGGATAGCAAAACAACTAGAAAATACATACAAAGATATATCAAGTTCTC 606
QY 201 CysLysGlnIleLysAsnIleAspIleValLysAsnValTyrThrLysAsnPheIle 220
DB
DB 607 TGTAAAGATATATATATATATATATATATATATATATATATATATATATATATATATAT 666
QY 221 ProPheMetAspSerLeuGluValIleSerAsnGlyLeuPheGluValIleAsnLeu 240
DB
DB 667 TTTTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 726
QY 241 SerLysArgTyrGluGluIleCysLeuLysAsnLysAspLeuAspAlaGluLeuPheLeu 260
DB
DB 727 TCTAAACATACGAGAAATTTATCTTTAAATAAAGATACATACATACATATATATATAT 786
QY 261 AspHisAspLysThrLeuGluIleAspSerIleAspSerPheGluThrGlnArgThrPro 280
DB
DB 787 GATCATATATATATATATATATATATATATATATATATATATATATATATATATATAT 846
QY 281 ArgLysSerAsnLeuAspGluValAsnValIleCysProHisThrProValArgThr 300
DB
DB 847 GAAAGAAATATATATATATATATATATATATATATATATATATATATATATATATAT 906
QY 301 ValMetAsnThrIleGlnGlnLeuMetIleLeuAsnSerAlaSerAspGlnProSer 320
DB
DB 907 GTTATGACATATATATATATATATATATATATATATATATATATATATATATATATAT 966
QY 321 GluAsnLeuIleSerCysPheAsnAspGluValAsnProLysLysLeuLys 340
DB
DB 967 GAAAGTATATATATATATATATATATATATATATATATATATATATATATATATATAT 1026
QY 341 ArgValLysAspIleCysGlyTyrIlePheLysGluLysPheAlaLysValGlyClnGly 360
DB
DB 1027 AGATGAGGATATATATATATATATATATATATATATATATATATATATATATATAT 1086
QY 361 CysValGlyIleGlySerGlnArgTrpLysLeuGlyValArgLeuTyrTrpArgValMet 380
DB
DB 1087 TGTGTCACATCTGCGGAGTGTGAGTATGCGGAGTATATATCAAGAGTATATCTTAAAG 1146
QY 381 GlnSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeu 400
DB
DB 1147 GATCATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1206
QY 401 AsnAspAsnIlePheHisMetSerLeuAlaCysAlaLeuGluValValMetAlaThr 420
DB
DB 1207 AATCATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1266
QY 421 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIle 440
DB
DB 1267 TATACACAGTACATCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCTGCAATCT 1326
QY 441 LeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLys 460
DB
DB 1327 CTGATATCTTAAATTTAAAGGCTTTGATTTTAAAGGCTTTGATTTTAAAGGCTTTTAA 1386
QY 461 AlaGlyGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgGlyGluHisArgIle 480
DB
DB 1387 GATCAAAAGTATATATATATATATATATATATATATATATATATATATATATATATAT 1446
QY 481 MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuLysGlnSerLys 500
DB
DB 1447 ATGCAATCTCTGCAATCTCTGCAATCTCTGCAATCTCTGCAATCTCTGCAATCTCTGCA 1506
QY 501 AspArgGlyGlyProThrArgHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 520
DB
DB 1507 GATCAAAAGTATATATATATATATATATATATATATATATATATATATATATATATAT 1566
QY 521 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysGly 540

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1667 AATAAAGACACGACATATGATCTTTCTGCTGTAAGATCTCCAAAGAAAAAAGGT 1626
541 SerThrThrArgValAsnSerThrAlaAsnAlaIleuThrAlaThrSerAlaIleuGln 560
1627 TCAATACAGGCTAAATCTACTGCAAAATGCAAGACACAAAGCAACATCAAGCTTCAG 1686
561 ThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 580
1687 AATCAACAAACCAATTCGAAATCACTGCTGCTTCACTGCTTCAAAAAAAGCTATCCGCTA 1746
581 AlaTyrLeuArgLeuAsnThrLeuTyrSerGluArgLeuLeuSerGlnLysProGluLeuGln 600
1747 GCTATCTGGGCTAAATACACTTTGTGAACGGCTTCTGCTGAGACAGCTAGAAATTAGAA 1806
601 HistLeuLeuPheThrLeuPheGlnHisThrLeuGlnAsnGlnTyrGlnLeuMetTargAsp 620
1807 CAATCATCTGACACATCTTTGACACACACACACACACACACACACACACACACACAC 1866
621 ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIle 640
1867 AATCAATTCGACCAAAATTAACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1926
641 AspLeuLysPheLysIleValThrAlaTyrLysAspLeuProHisAlaValGlnGln 660
1927 GACTTAAATTCAAATCATTTGATACACATACACAGATCTCTCTCATGTTGTTCAAGAG 1986
661 ThrPheLysArgValLeuIleLysIleGlnTyrAspSerIleIleValPheTyrAsn 680
1987 AATTCAAAAGTGTTTGTATCAACACACACACACACACACACACACACACACACACAC 2046
681 SerValPheMetGluArgLeuLysThrAsnIleLeuGlnIleTyrAlaSerThrArgProPro 700
2047 TGGCTGCTGACACACACACACACACACACACACACACACACACACACACACACACAC 2106
701 ThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSerSerProLeu 720
2107 AATTGCTACCAATATCTCATCTGCTGACACACACACACACACACACACACACACACAC 2166
721 ArgIleProGlyTyrAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGlu 740
2167 CAGATCTGACACACACACACACACACACACACACACACACACACACACACACACAC 2226
741 GlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGlu 760
2227 GCTGCTGCAACACACACACACACACACACACACACACACACACACACACACACACAC 2286
761 SerPheGlyThrSerGlnLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArg 780
2287 TCAATGCGACTTCTCAGAAATTCACCAATTAATCAATCAATCAATCAATCAATCAATCA 2346
781 ValLeuLysArgSerAlaGlnGlySerAsnProProLysProLeuLysLysLeuArgPhe 800
2347 GCTATCAAAAGCAAGTGTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2406
801 AspIleGlySerAspGlnAlaAspGlySerLysHisLeuProGlyGlnSerLysPhe 820
2407 GATATGAGAGCAACATCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 2466
821 GlnGlnLysLeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsn 840
2467 CACACCAAAATGCGCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2526
841 AspSerMetAspThrSerAsnLysGlnLysLys 861
2527 GATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2587
PSEUT 2
AAQ04713
ID AAQ04713 standard; CHINA; 2994 BP.
XX
AC AAQ04713
XX

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DT 11-OCT-1990 (first entry)
XX
DE Cancer suppressing gene (CSG).
XX
KW Cancer; cancer suppressing gene; CSG; 1q14; retinoblastoma;
KW RB; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 139..2922
FT /*tag= a
XX
PN W09005180-A.
XX
PD 17 MAY-1990.
XX
PE 30 OCT-1989; 89W000480H.
XX
PR 31 OCT 1988, 8803 0245829.
XX
PA (REGC ) UNIV OF CALIFORNIA.
XX
PI Lee WH, Huang HJS;
XX
DR WP1; 1990-178822/23.
DR P PSDB; AAK05405.
XX
PT Controlling cancer
PT by replacing ineffective cancer suppressing gene with cloned,
PT active gene.
XX
PS Claim 35; Page 86; 105pp; English.
XX
CC Gene is taken from human chromosome 1q14 retinoblastoma (RB) cDNA.
CC By installing a working CSG, rate and specific treatment and
CC prophylaxis can be given to cancer patients.
XX
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T; 0 other;

Alignment Scores:
Pred. No.: 0 Length: 2994
Score: 4467.00 Matches: 850
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 11 Gaps: 0

US-09-026-459A-33 (1-851) x AAQ04713 (1-2994)

QY 2 GlnLysValSerSerValAspGlyValLeuGlyTyrIleGlnLysLysLysLeuLeu 21
DB 373 GACAAAGATTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 442
QY 22 TptGlyIleCysIlePheIleAlaAlaValAspLeuAspGlnMetSerPheThrPheThr 41
DB 433 TGGGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 492
QY 42 GlnLeuGlnLysAsnIleGlnIleSerValHisLysPheAsnLeuLeuLysLeuLeu 61
DB 493 GACTACAGAAAAACATGAAATAGTGTCTTAAATTTTAAATTAAATAAAATAATT 562
QY 62 AspThrSerThrLysValAspAsnAlaMetSerAlaLeuLeuLysLysLysLysLysValLeu 81
DB 553 GATACCACTACCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 612
QY 82 PheAlaLeuPheSerLysLeuGlnArgThrGlySerGlnLeuIleTyrLeuThrGlnProSer 101
DB 613 TTTCACACTCTTCAGCAAAATTCGAAAGCAATGCTGCAACTTAAATATATATATATATAT 672
QY 102 SerSerIleSerThrGlnIleAsnSerAlaLeuValLeuLysValSerThrIleThrPhe 121
DB 673 AGTTGATATCTCTGAAATAAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 742

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Db 2894 AGATGCAATATGTTTAAATGAGAGAGAA 2922
RESULT 4
AA041545
XX AA041545 standard: DNA: 2994 bp.
XX AA041545
XX 24 AUG 1994 (first entry)
XX
XX Retinoblastoma gene.
XX
XX RB gene product: p56kb portion; cell cycle progression control;
XX combination: therapeutic methods: arrest; tumorigenesis;
XX regulation: physiological processes; blood cell prodn.;
XX quante prodn.: ss.
XX
XX Homo sapiens SR 40 cell line.
XX
XX Key Location/Qualifiers
XX CDS 139..2925
XX F1 /*F1: 4
XX F4 /note: "Rb protein"
XX
XX W090826.7 A.
XX
XX 29 APR 1994.
XX
XX 16 Oct 1992: 9200 GS08914.
XX
XX 17 Oct 1991: 9105 0778510.
XX
XX (RG97) UNIV CALIF/ENIA.
XX
XX Goodrich HW. Lee EYHP. Lee WH. Wang NP.
XX
XX W013 1993 152462/18.
XX
XX P psq46: AB066544
XX
XX Method of controlling cell cycle progression: uses purified
XX retinoblastoma protein or fragment, for use in combination with
XX therapeutic methods to arrest tumorigenesis
XX
XX Disclosure: Fig 9; 68pps: English.
XX
XX The sequence is that of the retinoblastoma gene which encodes the
XX retinoblastoma (Rb) protein which may be used as part of a method of
XX controlling cell cycle progression which may be used in combination
XX with therapeutic methods to arrest tumorigenesis in organisms. The
XX cell cycle can be reversibly arrested in a convenient and safe
XX manner. The protein is used in a compsn. is relatively inexpensive
XX and readily obtainable, and shows little or no toxic effects on
XX healthy cells. It is also compatible with other methods and devices
XX for regulating certain physiological processes of the body, such as
XX blood cell prodn. and dmate prodn. Fragments of the protein are
XX soluble in low concns. of glycerol thus enhancing their value in
XX pharmaceutical applications.
XX
XX Sequence 2994 bp: 974 A; 618 C; 594 G; 808 T; 0 other;
XX
XX Alignment Scores:
XX
XX Seq. No.: 0 Length: 2994
XX Scores: Matches: 850
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 99.89% Indels: 0
XX 14 Gaps: 0
XX
XX US 09 026 459A 33 (1 851) x AA041545 (1-2994)
XX
XX 2 ChdLysValSerSerValAspGlyValLeuGlyTyrTleGlnLysLysLysChdLys 21
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

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Db 373 GAGAAAGTTCATCTGCAATGACGATATGCAAGCTTATAATCTAAAAACAAAAAATAATG 432
QY 22 TTPGCTTLeCysTLePheTLeAlaValAspLeuAspGluMetSerPheThrPheThr 41
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Db 433 TGGGGAATCTGATCTTATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
QY 42 GluLeuGlnLysAsnTLeGlnTLeSerValHisLysPhePheAsnLysLeuTLe 61
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Db 494 GAGCTACAGAAAAATAGAAAAATAGTGTCCATAAAATCTTTAACTTAACTTAACTTAACT 592
QY 62 AspThrSerThrLysValAspAspAlaMetSerAlaLeuLeuLysLysLysTLeAspValLeu 81
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Db 553 GATACAGAACAAAGTTCATATGCTATGTCAGACAGCTTTCAGAAACAAAGAGAGAGAGAG 612
QY 82 PheAlaLeuPheSerLysLeuGlnAratLysLysLysLysLysLysLysLysLysLys 101
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Db 614 TTTCGACCTTCAGCAAAATGCAAGAGACATGTGAACTTATATATATATATATATATATAT 672
QY 102 SerSerTLeSerThrGlnTLeAsnSerAlaLeuValLysValSerTLePheThrPhe 121
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Db 673 AGTTGATATCTACTGAAATAAAATCTGATTGCTGTAAAGTTCCTTGATGATGATTT 742
QY 122 LeuLeuAlaLysGlyLysLysValLeuGlnMetGluAspAspLeuValLysSerPheGlnLeu 141
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Db 733 TTATAGCTAAAGGGAGAGATATACAAAGCAAGATGATCTGGGATATATATATATATAT 792
QY 142 MetLeuCysValLeuAspTyrPheTLeLysLeuSerProPrometLeuLeuLysLysPro 161
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Db 794 ATGCTATGCTGCTTGAATATTATTATTAAGCTCTACGCTCTGCTCTCTCTCTCTCTCTCT 892
QY 162 TyrLysThrAlaValTLePheTLeAsnLysSerProAratThrProAratGlyLysLeuAsn 181
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Db 853 TATAAACAAGTGTATATAGCTTAAATGCTTCACTGCTCAAACTGCTCAAACTGCTCAAACT 912
QY 182 ArgSerAlaAratLeuAlaLysGlnLeuLysGlnLeuLysGlnLeuLysGlnLeuLysGln 201
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QY 202 LysGlnLysGlnCysAsnTLeAspGlnValLysAsnValTyrPheLysAsnLysLysPro 221
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QY 222 PheMetAsnSerLysGlyLeuValThrSerAsnLysLeuProGlnValGlnAsnLysSer 241
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QY 262 HisAspLysThrLeuGlnThrAspSerTLeAspSerPheGlnThrGlnAratGlnPheArat 281
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QY 282 LysSerAsnLeuAspTLeGlnValAsnValTLeSerTLeSerTLeSerTLeSerTLeSer 301
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Db 1213 AAAGATAACTTGAATGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1272
QY 302 MetAsnThrTLeGlnLysLeuMetMetTLeLeuAsnSerAlaSerAspTLeProSerGln 321
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Db 1273 ATGCAACACTATGCCAACTAAATAAGATGATTTAAATACGCAAGTGAAGCTTCTTAA 1332
QY 322 AsnLeuTLeSerTyrPheAsnAsnGlyThrValAsnProLysGlnSerTLeLeuLysArat 341
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Db 1333 AATCTGATTTTCTATTTTAACTGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1392
QY 342 ValLysAspTLeGlyTyrTLePheTLeLysGlnLysPheAlaValGlyGlnGlyCys 361
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Db 1393 GTGCAAGGATATAGGATATATCTTTAAAGAGAAATTTGTAAAGTGTGGGTAAGAGGTTGT 1452
QY 362 ValGlnLysCysGlnAratTyrLysLeuGlyValAratLeuTyrTyrAratValMetGln 381
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Db	1493	 AATACATCTGACACATATGCTATCTCTGCTGAACATCTCCCAACCAAAACAGTTCAC	1592
Qy	542	 ThrThrArvValAsnSerThrAlaAsnAlaGlnThrGlnAlaThrSerAlaPheGlnThr	561
Db	1993	 ACTACCCGCTGTAATCTCTACTCCAAATCCAGACACACAGCAACCTCAGGCTTCCAGACG	2052
Qy	562	 GlnAlaSerProLeuLysSerThrSerLeuSerLeuPheCysLysValTyrArgLeuAla	581
Db	2053	 CAGAAGCATTTAAATCTATCTCTTTCACTGTTTATATAAAAAGTGTATCGGTAGCT	2112
Qy	582	 TyrLeuArgLeuAsnThrLeuGlnCysGlnArgLeuLeuSerGluHisProGlnLeuGlnHis	601
Db	2113	 TATCTCTGCTGTAATACAACTTCTCAAGGCGCTCTCTGTCAGCCACCACAAATACACAA	2172
Qy	602	 IleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlnTyrGlnLeuMetArgAspArg	621
Db	2173	 ATATCTGGACCGCTTCTCCAGCACACCTCCAGAAACAGTACATGAGCTCACAACATACC	2232
Qy	622	 HisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValIleAsnIleAsp	641
Db	2243	 CATTTTCATCAAAATATATATATCTCTGATCTGATCTGATATCTAATCTAATGATATAG	2302
Qy	642	 LeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGlnThr	661
Db	2293	 CTTAATATCAAAATCATGTAACACCAACAGAGATCTTCTCTCACTGCTGTTCAGGACACA	2352
Qy	662	 PheLysArgValLeuLysGlnGlnTyrAspSerIleIleValPheTyrAsnSer	681
Db	2353	 TTCAAACTGCTGTCTATCAAAACAGAGATGATGATCTATATAGTATCTATAAACTGG	2412
Qy	682	 ValPheMetCysArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProProThr	701
Db	2413	 GTCTTTATGTAAGATGTAATAATTTTGAGTAAGTCTCCACAGCGCGCTTACG	2472
Qy	702	 LeuSerProIleProHisIleProAlaGlnSerProTyrLysPheProSerSerProLeuArg	721
Db	2473	 TTCTCACTAATATCTCTCACAATCTCTGAACTCTTACAAAGTCTCTCACTCACTG	2532
Qy	722	 IleProGlnGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGlnGly	741
Db	2533	 ATTCTCTGGAGGAAATCTATATTTCACCCCTGAGAGTCCATATAAAATTCAGAAAGG	2592
Qy	742	 LeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGlnSer	761
Db	2593	 CTGTAAATATCAAAATAAAATATATCTCAATCAATGATCTTATGATCAATGGTGAATCA	2652
Qy	762	 PheGlyThrSerGlnLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgVal	781
Db	2653	 TCTGACATCTGCAGAACTTCAGAAAAATAATCAGATGGTATGTTAAACGCAACCGTGTG	2712
Qy	782	 LeuLysArgSerAlaGlnGlySerAsnProProLysProLeuLysLysLeuArgPheAsp	801
Db	2713	 CTCAAAAGATCTTCAAGCAACCAACCTCTCTTAACTCAGTCAAAAAACCTACCTTTCAT	2772
Qy	802	 IleGlnGlySerAspGlnAlaAspGlySerLysHisLeuProGlyGlnSerLysPheGln	821
Db	2773	 ATTCAAGATCATTAACATCATGCAATATAAATATCTCTGAGGAGAGTTCATAATTCA	2832
Qy	822	 GlnLysLeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAsp	841
Db	2833	 CATAAACTGCGAGAAATGACTTCTCTCTGACACACAGAAATGCAAAACGACAAAAATCA	2892
Qy	842	 SerMetAspThrSerAsnLysGlnGlnLys	851
Db	2893	 ACCATCGAATACCTCAAAACCAAGCAAGACAAA	2952
RESULT 9			
AA004474			
ID	AA004474	standard: cDNA: 2995 BP.	
XX	AC		
XX	AA004474:		

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462 ASFTSRThrIleValAspAlaMetSerArgLeuLeuLeuLysLysLysLysLysLysLys 81
463 TATAACAGATACAAATTTATATATATATATATATATATATATATATATATATATAT 480
464 theAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 101
465 TTTGACTCTTCAGCAATTCAGCAATTCAGCAATTCAGCAATTCAGCAATTCAGCAAT 540
466 SerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerThrIleThrPhe 121
467 AGTTCGATATCAGCAATTCAGCAATTCAGCAATTCAGCAATTCAGCAATTCAGCAAT 600
468 LeuLeuLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 141
469 TTTATTTGTTAAAGGAAATTTAAAGGAAATTTAAAGGAAATTTAAAGGAAATTTAA 560
470 MetLeuCysValLeuAspTyrPheIleLysLeuSerProMetLeuLeuLysGluPro 161
471 ATGATATGCTGTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 720
472 TyrLysThrAlaValIleProIleAsnGlySerProArgThrProArgArgGlyGluAsn 181
473 TATAAAGACCTGAT 780
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477 AAAAAGATGATGATTTATATATATATATATATATATATATATATATATATATAT 900
478 PheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuSer 241
479 TTTAGCAATCTCTGTGACTGTGTACATCTTAAAGGAAATTTAAAGGAAATTTAA 960
480 LysArgTyrGluGluIleCysLysLysLysLysLysLysLysLysLysLysLysLys 261
481 AAAAGATAGCAAAATTTATATATATATATATATATATATATATATATATATAT 1020
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489 AATCTGATTTCTCTATTTTAACTGACAGTGAATCCAAAGAGAGAGATATCTGAAAGA 1260
490 ValLysAspTyrGlyTyrIlePheLysLysLysLysLysLysLysLysLysLysLys 361
491 GTGAAGCAATAGCAAAATTTATATATATATATATATATATATATATATATATAT 1320
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494 SerMetLeuLysSerGluGluGluArgLeuSerIleGluAsnPheSerLysLeuLeuAsn 401
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497 GACAACATTTTTCAT 1500

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510 ThrThrArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAlaPheThrIle 561
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514 TyrLeuArgLeuAspThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGluHis 601
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516 IleIleThrThrLeuPheGluHisThrLeuGluAsnGluTyrGluLeuMetArgAspArg 621
517 ATCTCTGTAAATTTATTTAAATTCASAGACAAASACACCTCAGCTTCTCAGAGC 2100
518 HisLeuAspGluIleMetCysSerMetTyrClyLysLysValLysAsnIleAsp 641
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520 LeuLysPheLysIleValThrAlaTyrLysAspLeuProHisAlaValGluHisThr 661
521 CTAAATTTCAAAATTTGTAACAGCAATCAACCAATTTCTCTCATCTCTCTCAGCACA 2220
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 QY 542 ThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThr 561
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 DB 2041 ATCATGCAATGCTTTTCTAT 2100
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 QY 842 SerMetAspThrSerAsnLysGluLys 851
 DB 2761 AGCATGATATCTCAATCAAGGAAAGAGAA 2790
 RESULT 15
 AAA29391
 ID AAA29391 standard; DNA, 4839 BP.
 XX
 AC AAA29391;
 XX 12-SEP-2000 (first entry)
 XX Human retinoblastoma gene.
 XX hEST2, telomerase, catalytic subunit, reverse transcriptase; life-span;
 XX retinoblastoma; p53; tumour suppressor; inhibitor of telomerase;
 XX proliferation; immortal; tumour therapy; macular degeneration; activator;
 XX INK4, ss.
 OS Homo sapiens.
 XX W0200031238 A2.
 XX 02-SEP-2000.
 XX 24-NOV-1999; 99W0-US27907.
 XX 25-NOV-1998; 98US-0109891.
 XX 17-FEB-1999; 99US-0120549.
 XX (GENE-) GENETICA INC.
 XX Hannon GJ, Beach D;
 XX WPI; 2000-400055/34.
 PT New method for increasing the proliferative capacity of cell lines
 PT by administering agents reversibly activating telomerase
 PT activity and reversibly, transiently, inhibiting telomerase
 PT in treating age related diseases


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10 1942 AATACACTGACGACATATCTATCTCTCTGCTAAAGATCTCCAAAGAAAAAGCTTCA 1991*
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12 542 ThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThr 561
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14 1992 ACTAGCGGTGTAAATTTTATCTGTAAATGTAGAGAA'A'AA'AA'ALCAGGCTTCAGAGG 2051
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60 782 LeuLysArgSerAlaGlySerAsnProProLysProLeuLysLysLeuArgPheAsp 801
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62 2712 CTCAAAAGATGCTGAAGAAAG'AAAGTCTTAAAGCACTGAAAAATCTAGCTTTGAT 2771
63 |||
64 802 IleGlnGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPheGln 821
65 |||
66 2772 ATTGAAGATCAGATGAAG'AGATG'AAAGTAAATCTCTCCAGAGAGATCTCAAAATTCAG 2831
67 |||
68 822 GluLysLeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAsp 841
69 |||
70 2832 CAGAAACTGCCAGAAATCATCTCTACCCAGACAGCAATGCCAAAACCCAGAAAAATGAATGAT 2891
71 |||
72 842 SerMetAspThrSerAsnLysGluGluLys 851
73 |||
74 2892 AGCATGTATACCTCAAA'CAAGAGAGAAA 2921
```

Search completed: January 18, 2003, 08:39:18
Job time : 380.348 Secs

Genome version 5.1.3
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M nucleic nucleic search, using sw model

Run on: January 16, 2003, 15:29:17 : Search time 427.947 Seconds
(without alignments)
17531.794 Million cell updates/sec

Hit: US 09 026 459A 42
Perfect score: 3423
Sequence: 1 GGCATGACGAGAAAGTTTC.....AAATGACCATATATCATACT 3323

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searches: 2185209 seqs, 112599459 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum hit seq length: 0
Maximum hit seq length: 20000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	N.Geneset, 101002.*
1:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1980.DAT.*
2:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1981.DAT.*
3:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1982.DAT.*
4:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1983.DAT.*
5:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1984.DAT.*
6:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1985.DAT.*
7:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1986.DAT.*
8:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1987.DAT.*
9:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1988.DAT.*
10:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1989.DAT.*
11:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1990.DAT.*
12:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1991.DAT.*
13:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1992.DAT.*
14:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1993.DAT.*
15:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1994.DAT.*
16:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1995.DAT.*
17:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1996.DAT.*
18:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1997.DAT.*
19:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1998.DAT.*
20:	/S10S2/qp44a/a/geneset/geneset_emb1/NA1999.DAT.*
21:	/S10S2/qp44a/a/geneset/geneset_emb1/NA2000.DAT.*
22:	/S10S2/qp44a/a/geneset/geneset_emb1/NA2001.DAT.*
23:	/S10S2/qp44a/a/geneset/geneset_emb1/NA2002.DAT.*
24:	/S10S2/qp44a/a/geneset/geneset_emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	Hit ID	Description
1	3423	100.0	3423	AAV58443	Modified retinoblastoma
2	3415	99.8	3422	AAV58442	Modified retinoblastoma
3	3415	99.8	3455	AAV58441	Modified retinoblastoma
4	3415	99.8	3555	AAV58440	Modified retinoblastoma
5	3415	99.8	3555	AAV54940	DNA sequence of th
6	3415	99.8	4839	AAZ29301	Human retinoblastoma
7	3415	99.8	4839	AAZ88444	Human androgen rec
8	3415	99.8	4839	AAZ82874	Breast cancer rela
9	3413.4	99.7	4597	AAQ70546	Human retinoblastoma

10	3313.4	99.7	4597	20	AAU04501	Human retinoblastoma
11	3311.8	99.7	3594	19	AAV58452	Modified retinoblastoma
12	3311.8	99.7	4597	9	AAV58451	Human retinoblastoma
13	3280.8	98.7	4740	24	AAZ86079	Human retinoblastoma
14	3257.4	98.0	3266	19	AAV58444	Modified retinoblastoma
15	3237.4	97.4	4579	9	AAV58443	Probe for retinoblastoma
16	3226.6	97.1	3323	19	AAV58446	Modified retinoblastoma
17	3225.4	97.1	3461	19	AAV58447	Modified retinoblastoma
18	3212.4	96.7	3218	19	AAV54941	DNA sequence of th
19	3211.4	96.6	3243	15	AAQ72490	Retinoblastoma 94k
20	3107	93.5	3113	19	AAV58445	Modified retinoblastoma
21	3006	90.5	3347	19	AAV58448	Modified retinoblastoma
22	2956.6	89.0	3383	19	AAV58451	Modified retinoblastoma
23	2945.2	88.6	5056	10	AAV58449	CDNA of human retinoblastoma
24	2944.6	88.6	5377	19	AAV58450	Modified retinoblastoma
25	2827.4	85.1	3161	19	AAV58449	Modified retinoblastoma
26	2623	78.9	2994	11	AAQ34213	Cancer suppressor
27	2623	78.9	2994	14	AAQ41545	Retinoblastoma gene
28	2623	78.9	2994	19	AAV00004	Retinoblastoma protein
29	2623	78.9	2994	21	AAZ16287	Wild type human retinoblastoma
30	2620	78.8	2995	20	AAV58450	Human p110 RB retinoblastoma
31	2620	78.8	2995	20	AAV58450	Human p110 RB retinoblastoma
32	2620	78.8	2995	22	AAV58450	Human p110 RB retinoblastoma
33	2620	78.8	2995	22	AAV58450	Human p110 RB retinoblastoma
34	2620	78.8	2995	23	AAV58450	Human p110 RB retinoblastoma
35	2618.4	78.7	2995	16	AAQ86498	Human p110 RB retinoblastoma
36	2613.6	78.7	2995	16	AAQ86498	Human p110 RB retinoblastoma
37	835	25.1	18304	20	AAV04502	Human p110 RB retinoblastoma
38	831.8	25.0	18177	10	AAV04502	Human p110 RB retinoblastoma
39	220.8	6.6	1698	18	AAV2490	Antisense sequence
40	220.8	6.6	1802	18	AAV2490	Antisense sequence
41	220.8	6.6	2634	18	AAV2490	Antisense sequence
42	220.8	6.6	2634	18	AAV2490	Antisense sequence
43	220.8	6.6	2634	18	AAV2490	Antisense sequence
44	218.8	6.6	1697	16	AAV01542	Retinoblastoma protein
45	218.8	6.6	1697	16	AAV01542	Retinoblastoma protein

ALIGNMENTS

RES001 1	AAV58443 standard. DNA. 3423 bp.
AAV58443	
AC	AAV58443
XX	92-DEC-1998 (first entry)
XX	Modified retinoblastoma tumor suppressor gene.
XX	Modified retinoblastoma tumor suppressor, Rb protein cancer therapy.
XX	Cellular proteinase inhibitor.
XX	Homo sapiens.
XX	Key
XX	Location/Qualifiers
XX	7:2562
XX	/*tag- a
XX	W09837091-A2.
XX	27-AUG-1998.
XX	19-FEB-1998; 98W0-US04041.
XX	20-FEB-1997; 97US-0048118.
XX	(BAYU) BAYLOR COLLEGE MEDICINE.
XX	(TEXA) UNIV TEXAS SYSTEM.
XX	Benedict WF, Hu S, Xu H, Zhou Y.


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DB 2421 ATTCGGGACATTCGACAAAGCTGACAAATTAATACAGATGCTATGTAACAGTCAAGCGTGG 2480
QY 2449 GCTCAAAACAGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 2408
DB 2481 GTCAGAAACAGGCTCTGAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 2540
QY 2409 TATTCAGAAACAGGCTCTGAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 2468
DB 2541 TATTCAGAAACAGGCTCTGAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 2600
QY 2449 GCTCAAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 2528
DB 2601 GCTCAAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 2660
QY 2529 TATTCAGAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 2588
DB 2661 TATTCAGAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 2720
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DB 2721 TATTCAGAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 2780
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QY 2949 TATTCAGAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 3008
DB 3081 TATTCAGAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 3140
QY 3009 TATTCAGAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 3068
DB 3141 TATTCAGAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 3200
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DB 3381 TATTCAGAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 3440
QY 3309 TATTCAGAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 3368
DB 3441 TATTCAGAAACAGGCTCTAAGGAAAGCAAGCTCTTAACACATCTGAATAAAACATCTGTTGA 3500

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AAV58440
ID AAV58440 standard; DNA; 4555 bp.
XX
AC AAV58440;
XX
DI 02-DEC-1998 (first entry)
XX
DE Modified retinoblastoma tumour suppressor gene.
XX
KW Modified retinoblastoma tumour suppressor; RbP protein; cancer therapy;
cellular proliferation inhibitor; ss.
XX
OS Homo sapiens.
XX
FB Key Location/Qualifiers
FT CDS 7..2794
ET /misc_d
XX
W09837091-A2.
XX
PD 27-AUG-1998.
XX
PE 19-FEB-1998; 98W0-0503041.
XX
PR 20-FEB-1997; 97US 0038118.
XX
PA (BAYLOR COLLEGE MEDICINE.
PA (TEXAS) UNIV TEXAS SYSTEM.
PI Benedict WF, Hu S, Xu H, Zhou Y;
XX
DR WP1: 1998-480788/41.
DR P-PSDB: AAV69464.
XX
PT Retinoblastoma suppressor protein with N terminal modification
inhibiting cellular proliferation, particularly cancer.
XX
PS Discourse: Page 121-126; 249pp; English.
XX
CC This sequence encodes a modified retinoblastoma tumour suppressor
protein (RbP) of the invention. The proteins can be used for inhibiting
cellular proliferation, when coadministered with a p53 protein. The RbP
can be used for treating diseases characterized by abnormal cellular
proliferation, particularly cancers. The RbPs have a broader spectrum of
activity than wild type RbPs.
XX
SQ Sequence 4555 bp; 1171 A; 684 C; 653 G; 1047 T; 0 other;

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Query Match 99.8%; Score 3315; DB 19; Length 4555;
Rest Local Similarity 100.0%; Pctd. No. 0;
Matches 3315; Conservative 0; Mismatches 0; Labels 0; Gaps 0;
QY 9 GGAGAAATTTTCATCTGTGATGGATGATGGAGTTATATTCAGAAAGGAAAT 68
DB 240 CCAGAAATTTTCATCTGTGATGGATGATGGAGTTATATTCAGAAAGGAAAT 249
QY 69 GTGGGAAATCTGTATCTTTATTCAGAAATGATGATGATGATGATGATGAT 128
DB 300 GTGGGAAATCTGTATCTTTATTCAGAAATGATGATGATGATGATGATGAT 359
QY 129 TGAGTATAGAGAAATAGAGAAATGATGATGATGATGATGATGATGATGAT 188
DB 360 TGAGTATAGAGAAATAGAGAAATGATGATGATGATGATGATGATGATGAT 419
QY 189 TGATAGAGTATAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 248
DB 420 TGATAGAGTATAGAGTATGATGATGATGATGATGATGATGATGATGATGAT 479
QY 249 GTTTCAGTATCTTCAGAAATGAGAAAGCAAGCTCTTAACACATCTGTTGA 508
DB 480 GTTTCAGTATCTTCAGAAATGAGAAAGCAAGCTCTTAACACATCTGTTGA 549
QY 309 CAGTTCGATATCTACGAAATAGAAATGATGATGATGATGATGATGATGATGAT 368

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160 540 CAGTTCGATGCTACGACAAATAAAATTCGCGATGGTGGCTAAAGATTTCTGGGATCACATT 599
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1620 ACAATCCAACTTCACAGAGAGAAATGATAAAACAATTTAGAACGATGTCACAACTGAAATCAAT 1679
1649 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1508
1660 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1739
1689 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1568
1708 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1799
1727 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1628
1746 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1859
1765 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1688
1784 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1919
1803 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1748
1822 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1979
1841 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1808
1860 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2039
1879 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1868
1898 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2099
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1936 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2159
1955 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1988
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1993 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2048
2012 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2279
2031 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2108
2050 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2339
2069 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2168
2088 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2399
2107 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2228
2126 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2519
2145 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2348
2164 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2579
2183 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2408
2202 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2639
2221 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2468
2240 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2699
2259 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2528
2278 GGAATGCTTTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2759

10 600 TTATTAGCTAAGAGGAAAGTATTACAAATGGAAGATGATCTGCTGATTTCTTCAGTT 659
QY 429 AAATGCTAICHGCTGCTACATATTATTAATAACHTCTACCTGCCCAGCTGCTCAAGAACCC 488
Db 630 AATGCTAICHGCTGCTACATATTATTAATAACHTCTACCTGCCCAGCTGCTCAAGAACCC 719
QY 489 ATATATAACAGCTGCTTATAGCTGATTATAGCTTACCTGCGAANACCTGAGCGAGCTCAGAA 548
Db 720 ATATATAACAGCTGCTTATAGCTGATTATAGCTTACCTGCGAANACCTGAGCGAGCTCAGAA 779
QY 549 TATAGAGTCCAGCGAATAGCAAAACACCTAGAGAAATGATACAGAAATTTATCAAGCTTCCTG 608
Db 780 TATAGAGTCCAGCGAATAGCAAAACCTAGAGAAATGATACAGAAATTTATCAAGCTTCCTG 839
QY 609 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 668
Db 840 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 899
QY 669 TTTTATGAAATCTCTGCTGCTGCTTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
Db 900 TTTTATGAAATCTCTGCTGCTGCTTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
QY 729 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 788
Db 960 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1019
QY 789 TCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 848
Db 1020 TCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1079
QY 849 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 908
Db 1080 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1139
QY 909 TATGAACTATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 968
Db 1140 TATGAACTATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1199
QY 969 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1028
Db 1200 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1259
QY 1029 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1088
Db 1260 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1319
QY 1089 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1148
Db 1320 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1379
QY 1149 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1208
Db 1380 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1439
QY 1209 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1268
Db 1440 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1499
QY 1269 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1328
Db 1500 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1559
QY 1329 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1388
Db 1560 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1619
QY 1389 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1448
Db 1620 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1679
QY 1449 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1508
Db 1680 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1739

QY 1509 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1568
Db 1740 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1799
QY 1569 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1628
Db 1800 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1859
QY 1629 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1688
Db 1860 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1919
QY 1689 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1748
Db 1920 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1979
QY 1749 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1808
Db 1980 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2039
QY 1809 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1868
Db 2040 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2099
QY 1869 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1928
Db 2100 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2159
QY 1929 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 1988
Db 2160 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2219
QY 1989 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2048
Db 2220 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2279
QY 2049 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2108
Db 2280 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2339
QY 2109 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2168
Db 2340 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2399
QY 2349 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2228
Db 2400 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2459
QY 2329 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2288
Db 2460 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2519
QY 2389 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2348
Db 2520 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2579
QY 2349 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2408
Db 2580 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2639
QY 2409 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2468
Db 2640 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2699
QY 2469 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2528
Db 2700 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2759
QY 2529 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2588
Db 2760 TAAACACATCAATGATATAGCAAGGTCAGAAAATGTTTATTCAGAAAATTTATATACC 2819

DB 234 GGAGAAAGTTTCATCTGTCGAGGATATGGCAGGTATATTCACAAAGAAAAAGGAAC 293
QY 40 STARRAAATCTGATCTTTATATGACAGTTCAGTASATGAGATGCTGTCACCTTTAC 128
DB 294 STGGGAAATCTGATCTTTATATGACAGTTCAGTASATGAGATGCTGTCACCTTTAC 353
QY 129 TGAGTACAGAAAACATACAAATACAGTTCGATATATTCCTTTAACTTACTTAAAGAAAT 188
DB 354 TGAGTACAGAAAACATAGAAATCAGTTCGATATATTCCTTTAACTTACTTAAAGAAAT 413
QY 189 TCAATACAGTACCAAGTTCAGTATATGCTGTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 248
DB 414 TCAATACAGTACCAAGTTCAGTATATGCTGTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 473
QY 249 GTTTCAGTTCCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 308
DB 474 GTTTCAGTTCCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 533
QY 309 TCAATACAGTACCAAGTTCAGTATATGCTGTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 468
DB 534 TCAATACAGTACCAAGTTCAGTATATGCTGTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 593
QY 429 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 488
DB 594 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 713
QY 499 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 548
DB 714 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 773
QY 549 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 608
DB 774 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 833
QY 609 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 668
DB 834 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 893
QY 659 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 728
DB 894 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 953
QY 729 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 788
DB 954 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1013
QY 789 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 848
DB 1014 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1073
QY 849 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 908
DB 1074 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1133
QY 909 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 968
DB 1134 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1193
QY 969 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1028
DB 1194 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1253
QY 1029 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1088
DB 1254 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1313
QY 1089 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1148

DB 1314 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1373
QY 1149 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1208
DB 1374 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1433
QY 1209 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1268
DB 1434 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1493
QY 1269 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1328
DB 1494 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1553
QY 1329 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1388
DB 1554 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1613
QY 1389 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1448
DB 1614 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1673
QY 1449 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1508
DB 1674 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1733
QY 1509 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1568
DB 1734 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1793
QY 1569 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1628
DB 1794 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1853
QY 1629 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1688
DB 1854 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1913
QY 1689 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1748
DB 1914 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1973
QY 1749 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1808
DB 1974 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2033
QY 1809 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1868
DB 2034 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2093
QY 1869 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1928
DB 2094 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2153
QY 1929 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 1988
DB 2154 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2213
QY 1989 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2048
DB 2214 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2273
QY 2049 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2108
DB 2274 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2333
QY 2109 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2168
DB 2334 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2393
QY 2169 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2228
DB 2394 TATGATGCTGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 2453

[illegible]

QY	1329	GAATGTCGCTTAATTTTAAAGACCTTTGATGATTTTACAAAGTGATGCGAAGCTTTTATCAAAAGC	1388
Db	1330	TT	1389
Db	1360	GAATGTCGCTTAATTTTAAAGACCTTTGATGATTTTAAAGCTGATGCGAAGCTTTTATCAAAAGC	1619
QY	1389	AGAAAGCAATTTCCACAAAGCAAAATGATTAATAACATTTTAAGACGATGTGAATATCAAAATCAT	1448
Db	1620	ACAAAGCAAAATTTCCACAAAGCAAAATGATTAATAACATTTTAAGACGATGTGAATATCAAAATCAT	1679
QY	1449	GGAAATGCTTTGTAAGTGCTTCTGAGATTCACCTTTATTTTATGATCTTATTAATCAATCAAAAGTA	1508
Db	1680	GGAAATGCTTTGTAAGTGCTTCTGAGATTCACCTTTATTTTATGATCTTATTAATCAATCAAAAGTA	1739
QY	1509	CCGAGAAGGACCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1568
Db	1740	CCGAGAAGGACCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1799
QY	1569	TAAATACATATGTAAGTATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1628
Db	1800	TAAATACATATGTAAGTATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1859
QY	1629	AACTAGCGTGTAATTTCTTATGCAAGTACAGACAAAGCAAAAGTCAAGCTTCAGCTTCAGAACT	1688
Db	1860	AACTAGCGTGTAATTTCTTATGCAAGTACAGACAAAGCAAAAGTCAAGCTTCAGCTTCAGAACT	1919
QY	1689	CCACAAGCAATGAAATCTACGCTGCTTTCTACGCTTTTATATAAAACACGCTATGCGCTTACG	1748
Db	1920	CCACAAGCAATGAAATCTACGCTGCTTTCTACGCTTTTATATAAAACACGCTATGCGCTTACG	1979
QY	1749	CTATCTCGGACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1808
Db	1980	CTATCTCGGACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2039
QY	1869	TATATCTGCAATTTTCTTACAT	1868
Db	2040	TATATCTGCAATTTTCTTACAT	2099
QY	1869	GCATTTGCGACCAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1928
Db	2100	GCATTTGCGACCAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2159
QY	1929	CCCTTAATTCGAAATCATGCTATACAGCATATATATATATATATATATATATATATATATATATAT	1968
Db	2160	CCCTTAATTCGAAATCATGCTATACAGCATATATATATATATATATATATATATATATATATATAT	2219
QY	1989	ATTCAAAAGCTGTTTTTATCAATCAAGACAGAGATGATGATGATGATGATGATGATGATGATGATGAT	2048
Db	2220	ATTCAAAAGCTGTTTTTATCAATCAAGACAGAGATGATGATGATGATGATGATGATGATGATGATGAT	2279
QY	2049	CGCTGTCATGTCAGACACTGCAAAACAAATATTTTCCAGATGCTTCCATCAAGACGACGCGCTTAC	2108
Db	2280	CGCTGTCATGTCAGACACTGCAAAACAAATATTTTCCAGATGCTTCCATCAAGACGACGCGCTTAC	2339
QY	2109	CTTCTTACCAATATTTTATCAATCTGCGAAGCAATTTTAAAGTTCCTATGTTCAAGCTTCAAG	2168
Db	2340	CTTCTTACCAATTTTATCAATCTGCGAAGCAATTTTAAAGTTCCTATGTTCAAGCTTCAAGCTTCAAG	2399
QY	2169	GATTTCTGTAAGGAAAT	2228
Db	2400	GATTTCTGTAAGGAAAT	2459
QY	2229	TCTGCGTAACATCAACAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2288
Db	2460	TCTGCGTAACATCAACAAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	2519
QY	2249	ATTCGCAATTTTCTGAAATTTGCAAAATTAATATGAAATGATGATGATGATGATGATGATGATGATGAT	2348
Db	2520	ATTCGCGGACCTCTGCAAGATGCCAGAAAAATATAACAGATGCTATGCTATGCTATGCTATGCTATGCT	2579
QY	2349	GCTTCAAAAGAAAGTGCTGAAAGGAAGCAAGCTGCTATAAATCACTGCAAAAAAATAGAGTTTGA	2408
Db	2580	GCTTCAAAAGAAAGTGCTGAAAGGAAGCAAGCTGCTATAAATCACTGCAAAAAAATAGAGTTTGA	2639

2828 AAAATGCTGGCTTTATGGAATAGAAATGGGCTAGAGTGGAGTCTGTGATAGCCCA 2887
 4191 AAAATGGCTGGCTTTATGGAATAGAAATGGGCTAGAGTGGAGTCTGTGATAGCCCA 3250
 2888 GATGCTGTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 2947
 4251 GGGCTGTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3310
 2948 ATTAATTAATGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3007
 4311 ATTAATTAATGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3370
 4008 CTATGCTGTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3067
 4371 CTATGCTGTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3430
 4008 GATGCTGTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3127
 4451 GATGCTGTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3490
 4128 ATTAATTAATGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3187
 4491 ATTAATTAATGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3550
 4188 ATTAATTAATGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3247
 4551 ATTAATTAATGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3610
 4248 TATGCTGTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3307
 4611 TATGCTGTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3670
 4308 GATGCTGTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3423
 4671 GATGCTGTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 3686

RESULT 14
 AAV56444 standard; DNA: 4256 bp.
 AAV56444:
 02 DEC 1998 (first entry)
 Modified retinoblastoma tumour suppressor gene.
 Modified retinoblastoma tumour suppressor. Rb protein, cancer therapy.
 cellular proliferation inhibitor; ss.
 Homo Sapiens.
 Key
 CDS 7,250
 /ftag - 4
 W 08/05/91 AZ.
 21 AUG 1998.
 19 FEB 1998; 9800 US04041.
 20 FEB 1997; 9705 0048114.
 (RAY) BAYLOR COLLEGE MEDICINE.
 (TEXA) UNIV TEXAS SYSTEM.
 Homoduct WFL Hu S, Xu H, Zhou Y.
 WFL: 1998 480788/41.
 P PSDB: AAV69468.

PT Retinoblastoma suppressor protein with N terminal modification
 XX inhibiting cellular proliferation, particularly cancer
 PS Claim 22; Page 166-170; 24pp; English.
 XX This sequence encodes a modified retinoblastoma tumour suppressor
 CC protein (RbSP) of the invention. The protein can be used for inhibiting
 CC cellular proliferation, when coadministered with a p53 protein. The RbSPs
 CC can be used for treating diseases characterized by abnormal cellular
 CC proliferation, particularly cancers. The RbSPs have a broader spectrum of
 CC activity than wild type RbSPs.

SQ Sequence 3266 BP; 1092 A; 602 C; 574 G; 998 T; 0 other;

Query Match: 98.0%; Score 4257; DB 19; Length 4266;
 Best Local Similarity 100.0%; Pctid No. 0;
 Matches 3257; Conservative 0; Mismatches 0; Gaps 0;

QY 67 CTGTGGGAAATCGTATGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 126
 DB 10 CTGTGGGAAATCGTATGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 69
 QY 127 ACTGAGCTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 186
 DB 70 ACTGAGCTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 129
 QY 187 ATTGATGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 246
 DB 140 ATTGATGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 189
 QY 247 TTGTTTGGAGTCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 306
 DB 190 TTGTTTGGAGTCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 249
 QY 307 AGTCTGCTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 366
 DB 250 AGTCTGCTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 309
 QY 367 TTTTATTAGCTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 426
 DB 310 TTTTATTAGCTGATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 369
 QY 427 TTAATGCTATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 486
 DB 370 TTAATGCTATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 429
 QY 487 CCATATAAAGCAAGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 546
 DB 436 CCATATAAAGCAAGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 489
 QY 547 AACATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 606
 DB 490 AACATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 549
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 DB 790 CGAAAAATGATGCTGTGCTTTTGGAGCAATAGAGTGGAGTCTGTGATAGCCCA 849

XX W09847091 A2.
 XX ID
 XX 27 AUG-1998.
 XX
 XX 19 FEB-1998; 98W0-0503041.
 XX PR 20 FEB-1997; 97WS 0038118.
 XX (HAY) HAYLOR COLLEGE MEDICINE.
 XX (LFAA) UNIV TEXAS SYSTEM.
 XX
 XX Benedict WF, Hu S, Xu H, Zhou Y.
 XX W011998-480788/41.
 XX P 1998; AAW69366.
 XX
 XX Retinoblastoma suppressor protein with N-terminal modification -
 XX inhibition cellular proliferation, particularly cancer
 XX Title 22: Page 150-155; 94pp; English
 XX
 XX this sequence encodes a modified retinoblastoma tumour suppressor
 XX protein (RTPSP) of the invention. The proteins can be used for inhibiting
 XX cellular proliferation, when coadministered with a p53 protein. The RTPSPs
 XX can be used for treating diseases characterised by abnormal cellular
 XX proliferation, particularly cancers. The RTPSPs have a broader spectrum of
 XX activity than wild type RbSPs.
 XX
 XX Seq-no: 4592 BP; 1147 A; 614 C; 607 G; 1034 T; 0 other;
 XX
 XX Alignment Statistics:
 XX Pred. No.: 0 Length: 3392
 XX Score: 4504.00 Matches: 874
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX DB: 19 Gaps: 0
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 XX US 09-026-459a-31 (1-874) x AAW58442 (1-3392)
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 XX 427 TGGATACATTTTAT 486

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 31 3030 3
 32 AAU41545
 33 AAU41545 standard; tRNA; 2994 bp.
 34 AAU41545
 35 24 AUG 1993 (first entry)
 36 retinoblastoma gene.
 37 RB gene product: p56RB portion; cell cycle progression control;
 38 combination: therapeutic methods; arrest; tumorigenesis;
 39 regulation: physiological processes; blood cell prodn.;
 40 quonate prodn.; SS.
 41 Homo sapiens SR 40 cell line.
 42 K09 location/Qualifiers
 43 CDS 199..2925
 44 /note "RB protein"
 45 W09408267 A.
 46 29 APR 1993.
 47 16 OCT 1992: 9260 0808916.
 48 17 OCT 1991: 9105 0778516.
 49 (R032) -DNV CALIFORNIA.
 50 Genotech Inc. 100 KHP, 100 WB, 100 NP;
 51 W01, 1993 152462716.
 52 PFSDB; AAK0534.
 53 Method of controlled cell cycle progression: uses purified
 54 retinoblastoma protein or fragment, for use in combination with
 55 therapeutic methods to arrest tumorigenesis
 56 disclosed; Fig 9; 68pp; English.
 57 the sequence is that of the retinoblastoma gene which encodes the
 58 retinoblastoma (RB) protein which may be used as part of a method of
 59 controlling cell cycle progression which may be used in combination
 60 with therapeutic methods to arrest tumorigenesis in organisms. The
 61 cell cycle can be reversibly arrested in a convenient and safe
 62 manner. The protein is used in a compsn. is relatively inexpensive
 63 and readily obtainable, and shows little or no toxic effects on
 64 healthy cells. It is also compatible with other methods and devices
 65 for regulating certain physiological processes of the body, such as
 66 blood cell prodn. and cancer prodn. Fragments of the protein are
 67 soluble in low concns. of glycerol thus enhancing their value in
 68 pharmaceutical applications.
 69 Sequence 2994 bp; 974 A; 618 C; 594 G; 808 T; 0 other;
 70 Alignment Scores:
 71 Prod. No.: 0 Length: 2994
 72 Score: 4499.00 Matches: 874
 73 Percent Similarity: 100.00% Conservative: 0

Best local similarity: 100.00% Mismatches: 0
 Query Match: 99.89% Indels: 0
 DB: 14 Gaps: 0
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 22 LeuThrTrpLeuLysValSerSerValAspLysValLysLysLysLysLysLysLysLysLysLys 41
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 42 LysGlnLeuTrpGlyTleCysTlePheTleAlaAlaValAspLeuAspGlnMetSerPhe 61
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 82 LysGlnLys 101
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47 342 ProSerGluAsnGluSerThrPheAsnAsnCysThrValAsnProLysGluSerIle 361
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62 822 ArgPheAspIleGlyGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSer 841
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68
69 RESULT 4
70 AAV40004
71 ID AAV40004 standard; DNA; 2994 BP.
72 XX
73 AC AAV40004;
74 XX
75 15 FEB-1999 (first entry)
76 DE
77 DE Retinoblastoma protein RB.
78 XX
79 Retinoblastoma protein RB; E2F; transcription factor; human;
80 KW bladder cancer; osteoclast; angioplasty; diabetic retinopathy;
81 KW thyroid hyperplasia; Crave's disease; psoriasis;
82 KW benign prostatic hypertrophy; Li-Fraumeni syndrome;
83 KW peripheral vascular disease; therapy; ss.
84 XX
85 OS Homo sapiens.
86 XX
87 KEY Location/Qualifiers
88 CHS 149,12925
89 FT /*aa= a
90 XX
91 W09821228-A1.
92 XX
93 22-MAY-1998.
94 XX
95 13 NOV 1997; 97NOV-0521821.
96 XX
97 14-FEB-1997; 97FEB-0801092.
98 PR
99 15-NOV-1996; 96NOV-0751517.
100 XX
101 (CANU-) CANU1 INC.
102 XX
103 Anta Leon E, Gregory RJ, Wills KN.
104 XX
105 WPI; 1998-297858/26.
106 XX
107 P-PSDB; AAW62465.
108 DR

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47 342 ProSerGluAsnGluSerThrPheAsnAsnCysThrValAsnProLysGluSerIle 361
48 343 TATACCTGGCTCTTCATGTCAGAGACTGAAACAAATATTTTCAGTATGCTCCACAG 246
49 2404 TATACCTGGCTCTTCATGTCAGAGACTGAAACAAATATTTTCAGTATGCTCCACAG 246
50 722 ProProThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSerSer 741
51 723 TATACCTGGCTCTTCATGTCAGAGACTGAAACAAATATTTTCAGTATGCTCCACAG 246
52 2464 GGGCTTACCTTTCATGTCAGAGACTGAAACAAATATTTTCAGTATGCTCCACAG 246
53 742 ProLeuArgIleProGlyLysAsnIleTyrIleSerProLeuLysSerProTyrLysIle 761
54 743 TATACCTGGCTCTTCATGTCAGAGACTGAAACAAATATTTTCAGTATGCTCCACAG 246
55 2524 CCGTTAGAGATTCCTGGAGAGAAATCTATATTTTCAGTATGCTCCACAG 246
56 762 SerGlyGlyLeuProThrProHisMetThrProArgSerArgIleLeuValSerIle 781
57 2584 TCAGAGAGCTTTCATGTCAGAGACTGAAACAAATATTTTCAGTATGCTCCACAG 246
58 782 GlyGlySerPheGlyThrSerGlyLysPheGlyLysIleAsnGluMetValGlySerSer 801
59 2644 GCGCAATTCATTCGGGACTTCGACAAAGTTCCACAAATATTTTCAGTATGCTCCACAG 2703
60 802 AsnArgValLeuLysArgSerAlaGlyGlySerAsnProIleSerLeuLysSerLeu 821
61 2704 CAGCTGATGTTTAAAACAAATTCGAGGAGAGTAAAGGAGTAAAGTAAAGTAAAGTAA 2763
62 822 ArgPheAspIleGlyGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSer 841
63 2764 GCGTTTCATATTCAGAGATTCGACAAAGTTCCACAAATATTTTCAGTATGCTCCACAG 2823
64 842 LysPheGlyGlyLysSerAlaGlyMetThrSerThrArgMetGlyGlySerLeu 861
65 2824 AAATTCAGCAGAAATTCGACAAAGTTCCACAAATATTTTCAGTATGCTCCACAG 2883
66 862 MetAsnAspSerMetAspThrSerAsnLysGlyGlyLys 874
67 2884 ATGATATATATATATATATATATATATATATATATATATATATATATATATATAT 2922
68
69 RESULT 4
70 AAV40004
71 ID AAV40004 standard; DNA; 2994 BP.
72 XX
73 AC AAV40004;
74 XX
75 15 FEB-1999 (first entry)
76 DE
77 DE Retinoblastoma protein RB.
78 XX
79 Retinoblastoma protein RB; E2F; transcription factor; human;
80 KW bladder cancer; osteoclast; angioplasty; diabetic retinopathy;
81 KW thyroid hyperplasia; Crave's disease; psoriasis;
82 KW benign prostatic hypertrophy; Li-Fraumeni syndrome;
83 KW peripheral vascular disease; therapy; ss.
84 XX
85 OS Homo sapiens.
86 XX
87 KEY Location/Qualifiers
88 CHS 149,12925
89 FT /*aa= a
90 XX
91 W09821228-A1.
92 XX
93 22-MAY-1998.
94 XX
95 13 NOV 1997; 97NOV-0521821.
96 XX
97 14-FEB-1997; 97FEB-0801092.
98 PR
99 15-NOV-1996; 96NOV-0751517.
100 XX
101 (CANU-) CANU1 INC.
102 XX
103 Anta Leon E, Gregory RJ, Wills KN.
104 XX
105 WPI; 1998-297858/26.
106 XX
107 P-PSDB; AAW62465.
108 DR

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XX New fusion polypeptide (i.e., c.d. transfection factor) used to
 P1 treat c.d. hyper proliferative disease such as cancer and
 P2 restenosis.
 XX Example 1: F14 2A: 9LPP: English.
 XX This nucleotide sequence includes a coding region for retinoblastoma
 P3 protein RB (see AAW2455). A new claimed polypeptide is a fusion of:
 P4 (1) a transfection factor (TF) comprising a DNA binding domain,
 P5 and (11) a retinoblastoma (RB) polypeptide that includes a growth
 P6 suppression domain. Also new are: (1) a nucleic acid encoding the
 P7 fusion protein, and (2) expression vectors containing such DNA.
 P8 The fusion protein, particularly expressed from gene therapy
 P9 vectors (especially adenovirus vectors), is used to treat
 P10 hyperproliferative conditions, specifically cancer (particularly of
 P11 the bladder) or restenosis (after angioplasty), but also diabetic
 P12 retinopathy, thyroid hyperplasia, Graefe's disease, psoriasis,
 P13 benign prostatic hypertrophy, Li-Fraumeni syndrome and peripheral
 P14 vascular disease. Tissue-specific expression of E2Fp3 induces is
 P15 provided. The fusion proteins are more effective in repressing
 P16 transcription of the E2F promoter than RB alone and cause cell cycle
 P17 arrest in a variety of cells.

XX Sequence 2994 BP: 974 A; 518 C; 593 G; 809 T; 0 other;

Alignment Scores:

Prod. No.: 0 Length: 2994
 Score: 4499.30 Matches: 873
 Percent Similarity: 100.00% Conservatio: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.87% Indels: 0
 Gaps: 0

US 09 026 459A 31 (1 874) x AAW40004 (1-2994)

27 AspPheThrAlaLeuPheCysHisLysLeuLysLeuProAspHisValAcqHisArgAlaArg 21
 304 GATTTATAGTAAATGATGACAAATTAAGACATACCACACATGATGACAGACAGACCTGG 363
 22 LeuThrTrpCysValSerSerValAspValValLeuGlyClyTrpLeuHisLys 41
 364 TTAACTTGAGCAAAATTTTCATCTTGATGATGCAATATGACAGCTTATATTCAAAAGAA 423
 42 LysLeuLeuTrpCysLysLeuPheCysLeuAlaAlaValAspLeuAspGluMetSerPhe 61
 424 AAGAACCTGGGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483
 62 ThrPheThrGluLeuGlnLysAsnTLeGluLeuSerValHisLysPhePheAsnLeuLeu 81
 484 AATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
 82 LysGluLeuAspPheSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTrp 101
 544 AAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 603
 102 AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuLeuTrpLeuThr 121
 604 GATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 663
 122 GluProSerSerLysLeuSerThrGluLeuAsnSerAlaLeuValLeuLysValSerTrp 141
 664 AAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 723
 142 ThrPheLeuLeuAlaLysLysLysValLeuGluLeuMetGluAspAspLeuValLysSer 161
 144 AlaValTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 783
 162 PheLeuLeuMetLeuGysValLeuAspLysPheLeuLysLeuSerProGluMetLeuLeu 181
 784 TTTCAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 843
 182 LysGluPro-TyrLysThrAlaValLLePheProLeuAsnGlySerProArgThrProArgArg 201

844 AAAGAAACATATAAANAACCTGTTATACCTATTAAGGCTTAACTGAAACAAATGAGAGA 903
 202 GlyCysAsnSerValArgLeuAlaLysLysLeuLeuLeuAspGluPheAlaLeuLeuLeu 421
 904 GGTCAACAACAGAGGTGCAAGATAGCAAAACAAATACAAAATGATGATGATGATGATGATG 963
 222 ValLeuGysLysGluHisLysAsnLLeAspValValLysAsnValTyrPheLysAsn 241
 964 GTTCTGTAAGAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1023
 242 PheLeuProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGlu 261
 1024 TTATATGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
 262 AsnLeuSerLysSerValLeuLeuLeuLysLysAsnGysAspLeuAspAlaValGlu 281
 1084 AATCTTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143
 292 PheLeuAspHisAsnLysThrLeuGluLeuThrAspSerLLeAspSerPheGluThrLeuArg 301
 1144 TTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
 302 ThrProArgLysSerAsnLeuAspGluLeuValAsnValLLeProProHisLLeProVal 421
 1204 ACACCGCAAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
 422 ArgThrValMetAsnThrLeuGluLeuLeuMetMetLeuLeuAsnSerAlaSerAspHis 341
 1264 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
 442 ProSerGluAsnLeuLeuSerTyrPheAsnAsnGysThrValAsnProGlyHisSerLLe 361
 1324 CTTTCAGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383
 362 LeuLysArgValLysAsnLLeuLysTyrLeuPheLysLysLysPheAlaLysAlaValGly 381
 1384 CTGAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1443
 382 GlyCysValLeuLeuGlySerGluArgTyrLysLeuGlyValArgLeuTyrTyrArg 401
 1444 CAGGTGTGTGGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1503
 402 ValMetGluSerMetLeuLysSerLeuLeuGluArgLeuSerLLeGluAspPheSerLys 421
 1504 GATTTGGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1563
 422 LeuLeuAsnAspAspLLePheHisMetSerLeuLeuAlaLysAlaLeuGluValValMet 441
 1564 CTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1623
 442 AlaThrTyrSerArgSerThrSerGluAsnLeuAspGlyGlyThrAspLeuSerPhePro 461
 1624 GGCATATATAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
 462 TrpLLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValLLeuLysSerPhe 481
 1684 TGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1743
 482 LLeLysAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 501
 1744 ATCAAAAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG 1803
 502 ArgLeuMetGluSerLeuAlaLLeuLeuSerProGluPheAspLeuLeuLysLeu 521
 1804 GCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1863
 522 SerLysAspArgGlyGlyProThrAspHisLeuSerAlaLysLysLLeuAsnLeuPro 541
 1864 ICAAAAGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 1923
 542 LeuGluAsnAsnLysThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLys 561


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29 482 ThrGlyAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluAlaGlySerHisHis 501
10 1744 AATCAAAAGACAAAGGAAATTCAGAAACAAATTAAGAAATATTAAGAAATGACCAACAT 1803
29 502 ArgGluMetGluSerLeuAlaThrLeuSerAspSerProLeuThrAspLeuLeuLysGln 521
10 1804 CAAATCATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1863
29 522 SerGlyAspAlaGluGlyProThrAspHisGluGluSerAlaGlySerProLeuAsnLeuPro 541
10 1864 TCAAGGACGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1923
29 542 LeuGluAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValIleArgSerProLysLys 561
10 1924 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1983
29 562 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581
10 1984 AAGGCTTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2043
29 582 PheGluThrGlySerProLeuGlySerThrSerLeuSerLeuPheGlyTyrLysLysValTyr 601
10 2044 TCCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2103
29 602 ArgGluAlaTyrLeuAlaLeuAsnThrLeuGlySerAlaGlySerProGlnHisProGln 621
10 2104 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2163
29 622 LeuGluHisThrThrLeuLeuPheGluHisThrLeuGluAsnGluTyrGluLeuMet 641
10 2164 TTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2223
29 642 ArgAspArgHisLeuAspMetIleMetMetCysSerMetTyrGlyIleCysLysValLys 661
10 2224 AAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2283
29 662 AsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaVal 681
10 2284 AATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2343
29 682 GluGluThrPheGlyArgValLeuIleLysGluGluGlyTyrAspSerIleIleValPhe 701
10 2344 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2403
29 702 TyrAsnSerValPheMetGluThrAlaGluThrAlaGluThrAlaGluThrAlaGluThr 721
10 2404 TATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2463
29 722 ProGluThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSerSer 741
10 2464 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2523
29 742 ProGluArgGluProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysLys 761
10 2524 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2583
29 762 SerGluGlyGluProThrProThrLysMetThrProArgSerProTyrLysLeuValSer 781
10 2584 TCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2643
29 782 GlyGluSerPheGlyThrSerGlyLysPheGluGlyIleAsnGluMetValCysAsnSer 801
10 2644 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2703
29 802 ArgArgValLeuLysAlaGluGlySerAspArgProLysLysProLeuGlyGlyLeu 821
10 2704 GAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2763
29 822 ArgGluAspGluGluGlySerAspGluAlaAspGlySerLysHisGluProGlyLysSer 841
10 2764 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2823

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29 842 LysPheGluGlnLysLeuAlaGluMetThrSerThrThrArgMetGlnLysHisHis 861
10 2824 AAAATTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2883
29 862 MetAspAspSerMetAspThrSerAsnLysGlnGlnLys 874
10 2884 ATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2922
29 882 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 901
10 2924 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2983
29 902 ArgGluAlaTyrLeuAlaLeuAsnThrLeuGlySerAlaGlySerProGlnHisProGln 921
10 2984 AAGGCTTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3043
29 922 ArgGluAlaTyrLeuAlaLeuAsnThrLeuGlySerAlaGlySerProGlnHisProGln 941
10 3044 TTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3103
29 942 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 961
10 3104 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3163
29 962 AsnIleAspLeuLysPheLysIleIleValThrAlaTyrLysAspLeuProHisAlaVal 981
10 3164 AATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3223
29 982 GluGluThrPheGlyArgValLeuIleLysGluGluGlyTyrAspSerIleIleValPhe 1001
10 3224 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3283
29 1002 TyrAsnSerValPheMetGluThrAlaGluThrAlaGluThrAlaGluThrAlaGluThr 1021
10 3284 TATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3343
29 1022 ProGluThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSerSer 1041
10 3344 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3403
29 1042 ArgArgValLeuLysAlaGluGlySerAspArgProLysLysProLeuGlyGlyLeu 1061
10 3404 GAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3463
29 1062 SerGluGlyGluProThrProThrLysMetThrProArgSerProTyrLysLeuValSer 1081
10 3464 TCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3523
29 1082 GlyGluSerPheGlyThrSerGlyLysPheGluGlyIleAsnGluMetValCysAsnSer 1101
10 3524 CAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3583
29 1102 ArgGluAlaTyrLeuAlaLeuAsnThrLeuGlySerAlaGlySerProGlnHisProGln 1121
10 3584 AAGGCTTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 3643

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Alignment Scores:

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Pred. No.: 0 Length: 2995
Score: 4499.00 Matches: 874
Percent Similarity: 100.00% Conserved Pct: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.89% Indels: 0
EB: 22 Gaps: 0
95-99: 0.26 459A-31 (1-874) x AAH25755 (1-2995)

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29 2 AspheThrAlaLeuGlySerGlnLysGlnLysIleThrAspHisValAlaThrAlaGluThr 21
10 304 GATTTTATGATATATATATATATATATATATATATATATATATATATATATATATATATAT 363

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Recombinant adenovirus expression vector comprising a partial or total deletion of a protein IX DNA and a gene encoding a toxin protein e.g. suicide protein, useful for inhibiting or reducing the proliferation of a tumour e.g. brain tumour.

Disclosures: Fig 3; 3pp; English.

The present invention describes an adenoviral expression vector comprising a deletion in the protein IX gene and a gene encoding a toxin protein. This vector can be used in gene therapy, particularly to introduce tumour suppressor genes into cancerous cells. Genes which may be used include p53, thymidine kinase and retinoblastoma tumour suppressor gene (RB). The present sequence is the retinoblastoma tumour suppressor gene.

Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other.


```

222 ValLeuCysLysGlnHisGlyCysAsnHisAspGluValLysAsnValTyrPheLysAsn 241
DB 602 GTTCCTGCTGTAAAGAAATCAATATATAGATGAGTGTAAGATGTTATTTTCAAAAT 1023
QY 242 PheLeuProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGln 261
DB 2104 CAGCTAGCTATCTGCGGTAAATACACTTCTGCAATGCAATGCTGCTGCGAGCAACCA 2164
QY 622 LeuGluHisHisLeuThrPheLeuLeuHisThrLeuGluAsnGluTyrGluLeuMet 641
DB 2164 TTATGAAATATATATATATATATATATATATATATATATATATATATATATATAT 2223
QY 642 ArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyHisCysLysValLys 661
DB 2224 ACACACAGGCACTTCCACCAAAATATGATGATGATGATGATGATGATGATGATGATG 2283
QY 662 AsnIleAspLeuLysPheLysIleLeuValThrAlaTyrLysAspLeuProHisAlaVal 681
DB 2284 AATATAGAGCTTAAATTCAAATCAATGTAACAGCATACAAGGATCTTCCTCAAGCTG 2343
QY 682 GlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSerIleIleValPhe 701
DB 2344 CAGGAGCATTTTCAAAATGCTTTTATCAAAATGAGAGATATGATCTATATATATAT 2403
QY 702 TyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnIleTyrAlaSerThrArg 721
DB 2404 TATACTCGCTTCTCATGACAGACTGAAACAAATATTTCCAGTATGCTTCCACAGG 2463
QY 722 ProProThrLeuSerProIlePheProIleHisLeuThrArgSerProTyrLysPheProSerSer 741
DB 2464 CCCCCACCTTCTCACCATAACTTCACATTCCTGCAAGCCCTTACAAGCTTTCCTAGT 2523
QY 742 ProGluArgHisLeuGlyCysAsnIleTyrIleSerPheLeuLysSerProTyrLysIle 761
DB 2524 CATTATGAGTATTTGAGATGAAATATATATATATATATATATATATATATATATAT 2583
QY 762 SerGluGlyLeuThrProThrLysMetThrProArgSerArgIleLeuValSerIle 781
DB 2584 TCAGAGGCTGCTCCCAACCAACCAAAATGACTCCAGATCAAGAAATCTTAGATCAAT 2643
QY 782 GlyGluSerPheGlyThrSerGluLysPheGlyGlyAlaLeuAsnGluMetValLysAsnSer 801
DB 2644 GCGAATATCTCGGACCTTCATCAAGTTCACAGAAAATCAACATCAACATCAACATCA 2703
QY 802 AspArgValLeuLysArgSerAlaGluGlySerAsnProLysProLeuLysLysLys 821
DB 2704 CATCTGTGATTTAAAGAAATGCTTCAAGTTCACAGAAAATCAACATCAACATCAACAT 2763
QY 822 ArgPheAspIleGluGlySerAspGluAlaAspCysLysHisLeuProGlyGluSer 841
DB 2764 CGCTTCTCATATTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2823
QY 842 TyrPheGlnHisLysLeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLys 861
DB 2824 AAATTTCAACACAAACTTCCACAAATGCAATGCTTCACTCACTCACTCACTCACTCACT 2883
QY 862 MetAsnAspSerMetAspHisSerAsnLysGluGluLys 874
DB 2884 ATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2923

```

RESULT 10

ABL50904

ID ABL50904 standard: cDNA; 2995 BP.

XX ABL50904;

AC ABL50904;

DT 24-JUN-2002 (first entry)

XX Retinoblastoma tumour suppressor protein p110-RB encoding cDNA.

DE Retinoblastoma: tumour suppressor protein; p110-RB; cell cycle; p53;

KW PE; mitogen; cell death; adenoviral protein IX; gene therapy; cyclization;

KW adenovirus expression vector; tumour; non-small cell lung cancer;

KW small cell lung cancer; hepatocellular carcinoma;

QY	442	ProSerGlnAsnLeuTleSerTyrPheAsnAspCysThrValAsnProLeuSerHis	461
Db	1093	CTTTCAGAAAACTGCATTTCCTAATTTAAACACAGCAATGAAACAAAAAATAA	1152
QY	662	LeuGlyAsnValTyrAspGlnLeuGlyTyrThrPheCysGlnAspGlnPheAlaAsnAspValGly	681
Db	1153	CTGAAAAAGATCAAGATATAGATAATCTTTAAAGAGAAATTTGTTAAAGTTTGAGAA	1212
QY	482	GlnClyCysValGlnLeuLeuSerGlnAlaArgTyrLysGlnGlyValAlaGlnGlyTyrAla	401
Db	1213	CAAGGTGTGTGGAATTTGGATCAACAGATACAAATTTGAGATTGCTTCTATTACAA	1272
QY	402	ValMetGlnSerMetLeuLysSerGlnLeuAlaArgLeuSerHisGlnAsnPheSerLys	421
Db	1273	CTAAATGGCAATCAATCTTAAATCAGCAACAAACAAATATATCAATCAATCAATCAAT	1332
QY	422	LeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaLysAlaLeuGlnValValMet	441
Db	1333	CTTCTGAATCAACAAATTTTCATATGCTTTATTGGTGGTGGTCTTGAGGTCTAAAG	1392
QY	442	AlaThrTyrSerAspThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPhePro	461
Db	1393	GGCAATATATAGAGAAATGATCTCAAAATCTGATTTGGAAACAAATTTCTTTCTTCA	1452
QY	462	TrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValHisThrSerPhe	481
Db	1453	TGCAATCTCAATCTGCTTAAATTAAGACCTTTGATTTTAAACAGATGAGCAAACTTT	1512
QY	482	ThrLysAlaLeuAlaLysAlaLeuThrAlaGlnMetThrLysHisLeuAlaAspGlnHis	501
Db	1513	ATCAAAAGACAAAGGCAATTCGACAAACAAATGATGAAATTTTAAATGATGATGAT	1572
QY	502	ArgIleMetGlnSerLeuAlaIlePheSerAspSerProLeuPheAspLeuIleLysGln	521
Db	1573	CGAATCATGGAAATCGTTGATGGTCTCAATGTCATTTATTGATGCTATTAAACAA	1632
QY	522	SerLysAspArgGlnGlyProThrAspHisLeuAlaSerAlaLysProLeuAsnLeuPro	541
Db	1633	TCAAAAGACACAAAGGACCAACATCAATCTTCAATCTGCTGCTGCTGCTGCTGCT	1692
QY	542	LeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValAlaSerProLysLys	561
Db	1693	CTCCAGAAATATCACTGCACACATATGATCTTTCTGTGTAAAGATCTCAACAAAA	1752
QY	562	LysClySerThrThrArgValAsnSerThrAlaAsnAlaGlnThrGlnAlaThrSerAla	581
Db	1753	AAAGGTCACATACGGTGTGAAATTCATCTGAAAAAGACAAATCTAAATCTAAATCT	1812
QY	582	PheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysValTyr	601
Db	1813	TTCACACCCAGAAAGCAATCAAAATCAATCTCTCTTCACTGCTTTTAAAAAAGTGAT	1872
QY	602	ArgLeuAlaTyrLeuArgLeuAsnThrLeuGlyGlnAlaLeuLeuSerGlnHisPheAla	621
Db	1873	CGATCAAGCAATCTGGAGCTAAATTAATTTCTGAAAGATCTTCTCTGAAACAAAGAA	1932
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XX 09 MAY 2000 (first entry)
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XX Human androgen receptor coactivator: ARA54; ARA55; ARA24; detection;
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XX Bldm sapiens.
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XX
XX 27-JAN 2000.
XX
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XX
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XX 14-SEP 1998; 98US 0106243.
XX
XX (OYKP) UNIV ROCHESTER.
XX
XX Chomay C.
XX
XX W01: 2000 161130/14.
XX
XX P-PS00; AAY78421.

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XX
XX PT Novel androgen receptor associated proteins used to detect androgenic
XX PT or antiandrogenic activity in screening assays for candidate
XX PT pharmaceutical molecules which promote or inhibit the activity
XX
XX PS Claim 8; Page 47-53; 59pp; English.
XX
XX CC The present sequence encodes a human androgen receptor coactivator
XX CC designated Rb. Androgen receptor co-activator proteins from the
XX CC present invention can be used in screening assays to identify candidate
XX CC pharmaceutical molecules for the ability to promote or inhibit the
XX CC interaction of androgen receptors and androgen responsive elements to
XX CC modulate androgenic activity. The identification and characterization of
XX CC of androgen receptor co-activators such as those of the invention will
XX CC facilitate the development of screening assays to evaluate the potential
XX CC efficacy of drugs in the treatment of prostate cancer.
XX
XX SQ Sequence 4839 bp; 1544 A; 902 C; 880 G; 1524 T; 0 other;

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Alignment Scores:
Pred. No.: 0 Length: 4839
Score: 4499.00 Matches: 874
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 21 Gaps: 0
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1b 843 AAAGAAACCAATATAAACGCTCTTATATATCTGTCAGTATATGATATTCGTTTC 902
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Search completed: January 18, 2003, 08:37:31
Job time : 349,726 secs

GenCore version 5.1.1.4
Copyright (c) 1993-2003 CompuGen Ltd.

M protein: nucleic search, using frame_plus_p2n model

Run on: January 16, 2003, 23:41:58 : Search time 279.12 Seconds
(without alignments)
7011.240 Million cell updates/sec

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Scoring table:
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Ygapop 10.0 : Ygapext 0.5
Egapop 6.0 : Egapext 7.0
Delop 6.0 : Delext 7.0

Scatched: 218539 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	4454.5	98.9	2995	23	AAV50904
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12	4454.5	98.9	4849	21	AAV28844
13	4454.5	98.9	4849	24	AAV62873
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15	4446.5	98.8	2995	16	AAV06398
16	4445.5	98.7	2994	11	AAQ04713
17	4445.5	98.7	2995	20	AAV00737
18	4444.5	98.7	3554	19	AAV58441
19	4406.5	97.9	4740	24	AAV86079
20	4392	97.6	4597	15	AAV70036
21	4389	97.5	4597	20	AAV04501
22	4388	97.5	4597	9	AAV13069
23	4274.5	94.9	1579	9	AAV11291
24	4266.5	94.8	3455	19	AAV58441
25	4263	94.7	3461	19	AAV58447
26	4231	94.0	5056	10	AAV90489
27	4166	92.5	3383	19	AAV58451
28	4156.5	92.3	3392	19	AAV58442
29	4142	92.0	3357	19	AAV58438
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35	3849.5	86.5	3218	15	AAV54991
36	3674.5	81.6	4114	19	AAV58445
37	1854	41.2	18304	20	AAV04502
38	1759	39.1	18177	10	AAV0450
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45	516.5	11.5	3747	19	AAV05714

ALIGNMENTS

RESULT 1
AAV58450
15 AAV58450 standard; DNA, 3377 bp.

AC AAV58450:

DT 02-DEC-1998 (first entry)

DE Modified retinoblastoma tumour suppressor gene.

KW Modified retinoblastoma tumour suppressor RBP protein; cancer therapy;
cellular proliferation inhibitor; Src

CS protein sapiens.

XX key Location/Qualifiers

FT CDS 7..2616

FT /taq- a

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IDT 27-SEP-1999 (first entry)
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DE Human p110-RB retinoblastoma tumour suppressor encoding cDNA.
XX
KW Human; p110-RB; retinoblastoma; tumour suppressor; gene therapy;
KW adenoviral protein; IX; recombinant adenovirus expression vector;
KW cell cycle; p53; mitosis; cell death; apoptosis; thymidine kinase;
KW cancer; ss.
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XX
PH Ref Location/Qualifiers
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FT /note= "retinoblastoma tumour suppressor"
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XX
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 DB 2719 AGAAGTCTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2778
 QY 822 GlySerAspGlnAlaAspGlySerLysHisLeuProThrLysThrLysThrLys 841
 DB 2779 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2838
 QY 842 LeuAlaGlnMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 861
 DB 2839 CTGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2898
 QY 862 AspThrSerAsnLysGlnGlnLys 869
 DB 2899 CATATCTCAAAACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2922
 RESULT 9
 AAV58440
 ID AAV58440 standard: DNA: 4555 bp.
 XX
 AC AAV58440;
 DT 02 DEC 1998 (first entry)
 DE Modified retinoblastoma tumour suppressor gene.
 XX
 KW Modified retinoblastoma tumour suppressor; RbP protein; cancer therapy;
 XX cellular proliferation inhibitor; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..2794

462 LeuAsnLeuLysAlaPheAspPheTyrIysValIleGluSerPheIleIysAlaGluGly 481
 1567 TTTAAATTAAGAGTTCATTTTACAAAGTATACGAAAGTTTATCAAAAGCAGAGGC 1626
 482 AsnLeuThrArgGluMetIleLysHisGluGlnArgTyrSerHisAlaValIleMetGluSer 501
 1627 AATTGCAAGAGAAATATATAAATATTAGAGGATGTGAAATGCAATCATGGAAATCC 1686
 502 LeuAlaIleProLysAspSerProGluPheAspLeuIleLysIleSerTyrAspArgGlu 521
 1687 CTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1746
 522 GlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 541
 1747 GATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1806
 542 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThrThr 561
 1807 ATGAGAGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1866
 562 ArgValAsnSerThrAlaAsnAlaGlnThrGlnAlaThrSerAlaIleGlnThrGlnLys 581
 1867 CTTGTAATAATCTACTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1926
 582 ProLeuLysSerThrSerLeuSerLeuPheTyrIleLysValTyrArgLeuAlaTyrLeu 601
 1927 CATTGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1986
 602 ArgLeuAsnThrLeuCysHisArgLeuLeuSerGluHisProGluGluHisIleIle 621
 1987 CAGGTAAATATCTTGTGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 2046
 622 TrpThrLeuPheGlnHisThrLeuGlnAsnGlnIleGluLeuMetArgAspArgHisLeu 641
 2047 TGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2106
 642 AspGlnIleMetMetCysSerMetTyrGlyTyrCysLysValLysAsnIleAspLeuLys 661
 2107 GATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2166
 662 PheLysIleIleValThrAlaTyrIleAspLeuProHisAlaValGlnGlnThrPheLys 681
 2167 TTTAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2226
 682 ArgValLeuIleLysGluGlnIleGluArgSerIleIleValPheTyrAsnSerValPhe 701
 2227 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2286
 702 MetGlnArgLeuLysThrAsnIleLeuGlnIleTyrAlaSerThrArgProTyrLeuSer 721
 2287 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2346
 722 ProIleProHisIleProArgSerProLysPheProSerProLeuArgIlePro 741
 2347 GATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2406
 742 GlyLysAsnIleTyrIleSerProLysSerProLysIleSerGluGluLeuPro 761
 2407 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2466
 762 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGly 781
 2467 AATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2526
 782 ThrThrPheGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 801
 2527 AATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2586
 802 ArgSerAlaGluGlySerAsnProLysProLysLysLysLysLysLysLysLysLysLys 821
 2587 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2646
 822 GlySerAspGlnAlaAspLysSerLysHisProLysProLysProLysProLysProLys 841

2647 GATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2706
 842 LeuAlaGluMetThrSerThrArgIleThrArgMetGlnIleLysLysMetAspSerMet 861
 2707 CTGGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2766
 862 AspThrSerAsnLysGluGluLys 869
 2767 GATATCTCAAAATCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 2826
 RESULT 10
 AAV54990 standard: DNA: 4555 BP.
 XX AAV54990
 AC AAV54990;
 DT 26-NOV-1998 (first entry)
 XX
 DE DNA sequence of the specification.
 XX
 KW Minimal promoter; tetracycline responsive expression vector; TRV;
 KW transcriptional transactivation domain; TRV;
 KW tetracycline repressor protein; TRP; tetracycline operator;
 KW production, stable cell line; protein production;
 KW tumour suppressor protein; treatment; cancer; SS;
 XX
 QS Unidentified.
 FH Key Location/Qualifiers
 FT CDS 7..2793
 FT /*Id= a
 XX
 PN W09837185-A2.
 XX
 PD 27 AUG-1998.
 XX
 PF 19-FEB-1998; 98WO-US04092.
 XX
 PR 20-FEB-1997; 97US-0048755.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Bu S, Loathetis CJ, Xu H, Zhou Y;
 XX
 DR WPI:1998 480796/41.
 DR P-PSDB: AAW71354.
 XX
 PT New tetracycline responsive expression vectors used for the
 PT tightly controlled expression of genes, such as tumor suppressor
 PT genes for treating cancers
 XX
 PS Disclosure: Pages 145-150; 190pp; English.
 CC The present sequence appears in the specification, which describes a
 CC tetracycline responsive expression vector (TRV), which contains a
 CC sequence encoding a fusion protein comprising a transcriptional
 CC transactivation domain (TAD) operatively attached to a tetracycline
 CC repressor protein (RP). The first sequence operatively positioned
 CC downstream of a promoter. The vector also contains a cloning site
 CC operatively positioned downstream of a basal promoter comprising a
 CC tetracycline operator. The TRVs can be used to produce stable cell
 CC lines in which gene expression is tightly regulated by tetracycline.
 CC They can be used for the production of proteins such as tumor
 CC suppressor proteins which can be used for treating diseases characterized
 CC by abnormal cellular proliferation, particularly cancers.
 XX
 SQ Sequence 4555 BP; 1171 A; 684 C; 653 G; 1047 T; 0 other;
 Alignment Scores:
 Prod. No.: 0 Length: 4555
 Score: 4494.50 Matches: 867
 Percent Similarity: 93.54%

438 ATCTGATCTTTATTTGACAGAGTGTAACTATGATGAGATGCTGCTTATTTAGAGTA 497
 439 GlnLysAsnIleClnLysSerValHisLysPheAsnIleClnLysClnLysPheThr 140
 440 CAGAAAACAAIAGAAACAGGIGGCAIAAAATCTTTAACTTACIAAAGAAATTTGATACC 557
 441 SerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAla 160
 442 AGTAATAAAGGICATAAATCTTATGCAAGATCTGTGAAGAAAGIATCAATGATGTTGCA 617
 443 LeuPheSerLysLeuGlnArgThrCysGlnLeuIleLysLeuThrGlnProSer 180
 444 CTCTTCAGCAAAATTTGAAAGAGATGTAATGAACTTATATATTTGACATACCCAGAGCTGG 677
 445 Met ----- 181
 446 AIAATCTACGAAATAAAATCTGCAATGGCTGCTTAAAGCTTTCTTGGATCACAATTTTATTA 737
 447 ----- 181
 448 GCTAAAGAGCAATTAACAAATGCAAGATGATCTGGTGAATTTCAATTTCAATGCTTA 797
 449 ----- 181
 450 TGTATCTTTTAACTTTTATTTTAAATCTGCAATGCTGCAATGCTGCAATGCTGCAATGCT 857
 451 ValAlaValIleProThrLysGlnSerProArgThrProArgArgGlyGlnAsnArgSer 201
 452 ACAGATGATTAATCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAATG 917
 453 AlaArgIleAlaLysGlnLeuGlnAsnAspThrArgIleIleGlnValLeuCysLysGln 221
 454 GCAAGGATAGCAAAACAACTAGAAAAAGATCAAGAAATTAATCAAGATGCTGCTGCTGCT 977
 455 HisClnCysAsnIleClnCysGlnValHisAsnValTyrPheLysAsnIleIleClnPheMet 241
 456 CATGAATGATATATAGATGAGGTGAAAATGCTTTATTTTCAAAAATTTTATACCTTTATG 1037
 457 AsnSerLeuGlnLysValThrSerAsnGlyLeuProGlnValGlnAsnLeuSerLysArg 261
 458 AATCTGCTTGGACCTGTAAGATCTAAAGCACTTCCAGAGGCTTCAAAATCTTTCTAAAGCA 1097
 459 TyrGlnIleLysLeuLysAsnLysAspLeuAlaArgLeuPheLeuAspHisAsp 281
 460 TACAAACAAATTAATCTTAAATTAAGAACTGATGCAAGATATTTTGGATCATGAT 1157
 461 LysThrLeuGlnThrAspSerIleAspSerPheGlnThrGlnArgThrProArgLysSer 301
 462 AAAATCTCTCAGATGATCTATAGATGATTTTGAATATGAGAACACACACACACACACACAT 1217
 463 AsnLeuAspGlnGlnValAsnValIleProProHisThrProValArgThrValMetAsn 321
 464 AATCTGATCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1277
 465 ThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGlnAsnLeu 341
 466 ACTAATCAACAAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1337
 467 IleSerTyrPheAsnAsnCysThrValAsnProLysGlnSerIleClnLysArgValLys 361
 468 ATTCTTATTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1397
 469 AspIleClnLysIlePhePheLysGlnLysPheAlaValIleClnClnClnClnClnClnCln 381
 470 GATATAGATATATCTTAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1457
 471 IleClnSerGlnArgTyrLysLeuGlnValArgLeuTyrTyrArgValMetGlnSerMet 401
 472 AATGATCAACACATCAAACTTGGAGTTCCTTGTATTTACGAGATATGGAATGCAATCCATG 1517
 473 LeuLysSerGlnGlnArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsn 421
 474 GTTAAATCAGAAAGAAAGATATATGATCAAAATTTTATGAAATTTTATGAAATTTTATGAA 1577

422 IlePheHisMetSerLeuLeuAlaCysAlaLeuGlnValValMetAlaThrTyrSerArg 441
 423 ATTTTTCATATGCTTATTTATGCGGCTGGGCTCTTGAAGCTGTAAAGGCCACATATAGTACA 1637
 442 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProIleLeuAsnVal 461
 443 AGTAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAAT 1697
 444 LeuAsnLeuLysAlaPheAspPheLysValIleClnSerPheLysAlaClnCln 481
 445 CTAAATTTAAAGGCTTTGATTTTAAAGGATGATGATGATGATGATGATGATGATGATGATGAT 1757
 446 AsnLeuThrArgIleMetIleLysIleLeuGlnArgCysGlnHisArgIleMetGlnSer 501
 447 AACITGACACACACAAAGATGAAACATTTAGAACGATGACACACACACACACACACACAC 1817
 502 LeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGln 521
 503 CTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1877
 522 ClnProThrAspHisClnClnSerAlaCysProLeuAsnIleClnClnClnClnClnClnCln 541
 523 GGACCAACTGATCAGCTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1937
 542 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysLysSerThrThr 561
 543 ACTGACACACATATATGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1997
 562 ArgValAsnSerThrAlaAsnAlaClnThrGlnAlaThrSerAlaPheGlnThrGlnLys 581
 563 GCTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2057
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 603 CGCTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2177
 622 TrpPheLeuPheGlnHisThrLeuGlnAsnGlnTyrAsnLeuMetAlaAspArgGlnLeu 641
 623 TGAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2237
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 663 TTCAAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAA 2357
 682 ArgValLeuLysIleLysGlnGlnThrArgSerIleIleValPheTyrAsnSerValPhe 701
 683 GCTCTTTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAAT 2417
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 722 ProIleProHisIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 741
 723 CCAATAGCTCAGATCTGCTGAGAGGCTTACAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCT 2537
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 762 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleClnGlnSerPheGly 781
 763 ACACCAACAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2657


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CY 642 AsparticAcidMetLeuSerMetTyrTyrIleCysLysValLysAsnIleAspLeuLys 661
DB 2259 GAGCAAAATATGAGAGAGGCTCCATGTAAGGATATGCAAACTCAAGCAATATACACCTTAAA 2298
CY 662 PheLysIleIleValThrAlaTyrLysAspLeuProHisAlaValGlnGluThrPheLys 681
DB 2259 TTCAAAATCATTTTAAAGCATATAGATTTTCTTATCTTTTCAAGAGATATTCAAA 2358
CY 692 ArgValLeuIleLeuSerGlnGluGlySerAspSerIleLeuValPheTyrAsnSerValIle 701
DB 2359 GAGTTTGTATGCAAGAGAGAGATATGATTTATATATATATATATATATATATATATATAT 2418
CY 702 MetGlnArgLeuLysThrAsnIleLeuGlnIleTyrAlaSerThrArgProProThrLeuSer 721
DB 2419 ATGCAGACACTGAAATCAAAATATTTCCAGTATGCTTCCACCAGGCCCTTACCTTGCA 2478
CY 722 ProIleProHisIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 741
DB 2479 GCAATAGCTGACATTTCTGAGAGCCTTTCAGTTTCTAGTTTCACTTACGGATTCT 2538
CY 742 GlyValAsnIleTyrIleSerProLeuSerProTyrTyrIleSerGlnGluLeuPro 761
DB 2539 GGAGAGAGCATTTATATTTTACCTTCAAGAGTCCATATAAAATTTTCAGAGAGTCTGCA 2598
CY 762 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGly 781
DB 2599 ACACCAACAAAAAGACTCCAGATCAAGAAATCTTAGTATCAATTCCTCAATTCCTGG 2658
CY 782 ThrSerGlnLysPheGlnLysIleAsnGlnMetValCysAsnSerAspArgValLeuLys 801
DB 2659 ACTTCGAGAGTTCTAGAAAATATAATTCAGATGATATATTAACAGGAGAGTGTGTCTCAA 2718
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DB 2719 AGAAATGCTGAAGAGAAATACCTCTTAACCACTGAAAAACTACGCTTTGATATGAA 2778
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DB 2779 GCAATCAATCAAGCAGACAGTAAAGTAAACATCTCCACAGCAGCTCCAAAATTCAGCAGAAA 2838
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DB 2899 GATAATCAAAACAAAGGAAAGAAA 2922
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Search completed: January 18, 2003, 08:51:09
Job time : 395.12 secs

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 1399 GATATAGATAATGCTTTAAAGAAATTTGTAAGAGTGTGGACAGGGTGTGTGAA 1458
 384 IleGlySerGlnArgTyrIleGlyValArgGlyTyrTyrArgValMetGlnSerMet 403
 1459 ATGGCAATCAACGCAACAACTGGAGTTCCTTGAATACCCAGATGATGAAATCAAG 1518
 404 LeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsn 423
 1519 CTAAATCAGACAGCAACAGCAATCCCAATCAAAATTTACCAACATCTGAAATCATAAAC 1578
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 1579 ATTTTCATATGCTTTATTGCTGTGGCTCTTAAAGTTGTAAATGGTCATATATAGCAGA 1638
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 464 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluIle 483
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 2059 GATTCGAAATCTACCT 2118
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259 CACTGCT 318
 61 CysGlnLysLeuLysIleProAspHisValArgGluArgAlaIlePheLeuThrProGluLys 80
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 81 ValSerSerValAspGlyValLeuGlyGlyTyrIleGlnLysLysSerLeuIleuTrpCly 100
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 121 GlnLysAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThr 140
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 241 Thr-----GlySer----- 243
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 244 AsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArg 263
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 1099 TAAAGAAATTTATCTTAAAGAAATTAATGATGATGATGATGATGATGATGATGATGATG 1158
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 1159 AAACCTCTCTCAGATGATCTATACAGCTTTTGAACACACAGACACACACCAACCAAG 1218
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 1219 AAGCTTATCAACAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1278
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 1279 AATATCAACAAATTAATGATGATTTTAAATTCAGCAGAGTATCAACCTTCAGAAAATCTG 1338


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244 AsnSerLeuGlyLeuValThrSerAspGlyLeuProGluValGluAsnLeuSerLysArg 263
1039 AATCTCTGGACCTGGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1098
264 TyrGluGluLeuTyrLeuLysAspLysAspLeuAspAlaLeuLeuPheLeuAspHisAsp 283
1099 TACAAATAATTTATCTTAAATAATAAGATCTAGATGGAGATATTTTGGATGATGAT 1198
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1199 AAAATCTCTGAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1218
404 AsnLeuAspGluGluValAsnValLleProProHisThrProValArgThrValMetAsn 323
1219 AATCTCTGAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1278
324 ThrLleGluGluLeuMetLleLeuAsnSerAlaSerAspGluProSerGluAsnLeu 343
1279 AATCTCTGAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1348
444 LysSerTyrPheAsnAspGlyThrValAsnProGlySerLleLeuLysArgValLys 363
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464 AspLleGlyTyrLlePheLysGluLysPheAlaLysAlaValGlyGlyGlyLysValGlu 383
1399 GATATGATACATCTCTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1458
484 LysGlySerGluArgTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMet 403
1459 AATCTCTGAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1518
404 LeuLysSerGluGluGluArgLeuSerLleGluAsnPheSerLysGluLeuAsnAspAsn 423
1519 CTAAATTTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1578
424 LysPheHisMetSerLeuLeuAlaLysAlaLeuGluValValMetAlaThrTyrSerArg 443
1579 AATCTCTGAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1638
444 SerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPheProTrpLleLeuAsnVal 463
1639 AATCTCTGAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1698
464 LeuAsnLeuLysAlaPheAspPheGlyLysValLleGluSerPheLleLysAlaGluGly 483
1699 CTAAATTTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1758
484 AsnLeuThrArgGluMetLleLysHisLeuGluArgCysGluHisArgLleMetGluSer 503
1759 AATCTCTGAGATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1818
504 LeuAlaThrLeuSerAspSerProLeuPheAspLeuLleLysGluSerLysAspArgGlu 523
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544 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysGlySerThrThr 563
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564 ArgValAsnSerThrAlaAsnAlaGluThrGluAlaThrSerAlaPheGluThrGluLys 583
1999 CTAAATTTAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2058
584 ProLeuLysSerThrSerLeuSerLeuPheLysValTyrArgLeuAlaTyrLeu 603
2059 GATATGATACATCTCTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 2118

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RESULT 9

AAV58440

ID AAV58440 standard: DNA: 4555 bp.

XX AAV58440:

XX AAV58440:

XX 02 DEC 1998 (first entry)

DE Modified retinoblastoma tumour suppressor gene.

XX Modified retinoblastoma tumour suppressor: RBP protein: cancer therapy:

XX cellular proliferation inhibitor; ss.

XX Homo sapiens.

XX Key Loc: 130/Qualifiers

FT CDS 7..2794

1b 418 APTTGTATGTTTATTTGACGAGTIGAGCTAGATGACATGCTGCTACCTTTTACTGAGCTA 497
 2b 121 GlnLysAsnIleGlnIleSerValHisLysPhePheAsnLeuLeuLysGlnIleAspThr 140
 1b 419 CAGAAAAACATAGAAATACAGTGGCCATAAATCTTTAACTTACTTAAGAAATATGATACC 557
 2b 122 SerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysIleAspValLeuPheAla 160
 1b 420 AGTACCAAGATGTATATGATGTATGTATGATGATGATGATGATGATGATGATGATGATGAT 617
 2b 123 LeuPheSerLysLysLeuArgThrGlySerLeuLeuIleTyrIleThrGlnProSerSerSer 180
 1b 421 GTTTCACCAAAATGGAAAGACAGTGGTATATATATTTGACACAAACCCAGCAGTTCG 677
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 1b 422 AATGCTATGAAATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 737
 2b 125 AlaLysGlyGlnValLeuGlnMetGluAspAspLeuValIleSerPheGlnLeuMetLeu 220
 1b 423 GCTAAAAGGAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
 2b 126 CysValLeuAspTyrPheIleLysLeuSerProPheMetLeuLeuLysGlnProLys 240
 1b 424 GGGGCTTGACATATATATTAACATGCTACCTTCCATGCTGCTCAAGAACCATATAAA 857
 2b 127 Thr-----GlySer----- 243
 1b 425 ACGTGTATTATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 917
 2b 128 GCTAAGATAGCAAAACAACTAGAAATATGATACAAATAATTATTCAAGTTCTGTAAAGAA 977
 2b 129 CAAGAACTGATAATAACAGAGTCAAAAAATGTTTATTAACCTTTTATG 1037
 2b 130 AsnSerLeuGlyValThrSerAspGlyLeuProGlnValGlnAsnLeuSerLysArg 263
 1b 131 AATTTCTTGACATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1097
 2b 132 TyrGlnIleLysLysLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAsp 283
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 2b 134 LysThrLeuGlnThrAspSerIleAspSerPheGlnThrGlnArgThrProArgLysSer 303
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2b 148 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProIleIleLeuAsnVal 463
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13 DEC 2001.

40 MAY 2001: 2001w010516838.

05 JUN 2000: 2000j03 2094740.

05 JUN 2000: 2000j05 2095416.

18 SEP 2000: 2000s05 2481434.

20 SEP 2000: 2000s05 2486176.

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20 SEP 2000: 2000s05 2486445.

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22 SEP 2000: 2000s05 2485904.

22 SEP 2000: 2000s05 2485674.

25 SEP 2000: 2000s05 2485244.

25 SEP 2000: 2000s05 2485774.

25 SEP 2000: 2000s05 2485082.

25 SEP 2000: 2000s05 2485144.

25 SEP 2000: 2000s05 2485284.

26 SEP 2000: 2000s05 2485434.

27 SEP 2000: 2000s05 2485711.

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27 SEP 2000: 2000s05 2485403.

27 SEP 2000: 2000s05 2486434.

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02 OCT 2000: 2000s05 2487124.

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03 OCT 2000: 2000s05 2487454.

03 OCT 2000: 2000s05 2487584.

03 OCT 2000: 2000s05 2487604.

03 OCT 2000: 2000s05 2487604.

01 NOV 2000: 2000s05 2488674.

01 NOV 2000: 2000s05 2488644.

(AVAL) AVAL-N PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Harrihan S,

Support DR, Weaver Z,

WPI, 2002 180263/24.

Screening for anti-neoplastic agent involves exposing cells to a

chemical agent to be tested for anti-neoplastic activity, and

determining a change in expression of a gene of a signature gene set

claim 1; SEQ ID 1210; 44pp; English.

The present invention describes a method (M1) for screening for an

anti-neoplastic agent. The method involves exposing cells to a chemical

agent to be tested for anti-neoplastic activity, determining a change in

expression of at least one gene (G) of a signature gene set, where (G)

comprises a sequence (S) selected from 8447 sequences (given in A01664

to A016710), or is at least 95% identical to (S), where a change in

expression is indicative of anti-neoplastic activity. (1) has cytostatic

activity and can be used in gene therapy. M1 can be used for screening

an anti-neoplastic agent, and can be used for producing a product which

is the data collected with respect to the anti-neoplastic agent as a

result of M1, and the data is sufficient to convey the chemical

structure and/or properties of the agent. M1 can be used in the

treatment of cancer such as colon, breast, stomach, lung, thyroid,

CC oesophageal, ovarian, kidney, prostate or pancreatic cancer.
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumor.

XX Sequence 4849 BP; 1534 A; 902 C; 880 G; 1524 T; 0 Other;

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Score: 4447.50 Matches: 871
Percent Similarity: 94.86% Conserved: 0
Best Local Similarity: 94.86% Mismatches: 0
Query Match: 98.92% Indels: 57
DB: 24 Gaps: 2

US 09 026 459A-49 (1-871) x AM62873 (1-4849)

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138 AIGAG 197

21 ProAlaProProProProProProProProProProProProProProPro 40

198 CGGAG 257

41 AspleuProLeuValArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeu 60

258 GACCTGCT 417

61 CysGlnLysLeuLysPheProAspPheValArgLeuGluPheGluGluThrGluGlu 80

318 TGTAG 477

81 ValSerValAspPheValLeuGluGluGluGluGluGluGluGluGluGluGlu 160

378 GTTTCATCTGT 447

101 IleCysIlePheIleAlaValAspLeuAspGluMetSerPheThrPheThrGluLeu 120

438 ATCTGTATCTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 497

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558 AGTACCAAGTTGAT 617

161 LeuPheSerLysLeuGluArgThrCysGluLeuIleLysLeuThrGluProSerSer 180

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QY 824 GlySerAspGluAlaAspGlySerLysHisLeuPheGluSerLysPheGlnGlnLys 843
DB 2779 GGATGCAATATCAAGTATATGAAATAAAATATCTCTCTCTCTCTCTCTCTCTCTCTCT 2838
QY 844 LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 863
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QY 864 AspThrSerAsnLysGluGluLys 871
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RESULT 15
AAQ04713
ID AAQ04713 standard; cDNA; 2994 BP.
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AC AAQ04713;
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DT 11-OCT-1990 (first entry)
XX
DE Cancer suppressing gene (CSG).
XX
KW Cancer; cancer suppressing gene; CSG; 13q14; retinoblastoma;
RB; ds.
XX
OS Homo sapiens.
XX
KY Key
CDS 139..2922
Location/Qualifiers
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XX
PN W09005180-A.
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PE 17-MAY-1990.
XX
PF 30-DEC-1989; K4W0-000480R
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PR 31-OCT-1988; 8805 0265829.
XX
PA (HEG ) UNIV OF CALIFORNIA.
XX
PI Lee WH, Huang HJS.
XX
PS WP1: 2990-178832/23.
DB P-PSDB; AAR05305.
XX
PT Controlling cancer -
PT by replacing ineffective cancer suppressing gene with cloned,
PT active gene.
XX
PS Claim 35: Page 86; 105pp; English.
XX
CC Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
CC by installing a working CSG, safe and specific treatment and
CC prophylaxis can be given to cancer patients.
XX
SQ Sequence 2994 BP; 974 A; 618 C; 593 G; 809 T; 0 other;
Alignment Scores:
Proj No.: 0 length: 2994
Score: 4438.50 Matches: 870
Percent Similarity: 94.75% Conservative: 0
Best Local Similarity: 94.75% Mismatches: 1
Query Match: 98.72% Indels: 57
DB: 11 Gaps: 2
US-09-026-459a-49 (1-871) x AAQ04713 (1-2994)

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28 2839 CTGGCAAAAAAGACATCTACCTCCAAATACCAATGCCAAAAACAGAAATGCAATGATAGCAATG 2898
29 864 AspThrSerAsnLysGluLys 871
30 2899 GATACCTTAAACAAGGAGAGAGAA 2922
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(without alignments)
14944,909 million cell updates/sec

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722 ATAAATGAGAGTC----- 734
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734----- 734
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734----- 734
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1034 TATATGCTTGAATATTTTAAATGCAAGATGATCGGAGATTCATTTCAGTTAA 790
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734 AAGAAATGAGAGTC----- 850
1034 AAGAAATGAGAGTC----- 1153
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1034 AAGAAATGAGAGTC----- 1213
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1214 AAGAAATGAGAGTC----- 1273
974 AAGAAATGAGAGTC----- 1030
1274 AAGAAATGAGAGTC----- 1333
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1454 AAGAAATGAGAGTC----- 1870
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1814 AATCCCTTCAATGCTTCAAGATTCACCTTTATTTGATCTTATTAAACAAATCAAGAGAT 1873
1571 GATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1630
1874 GATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1933
1631 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1690
1934 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1993
1691 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1750
1994 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2053
1751 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1810
2054 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2113
1811 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1870
2114 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2173
1871 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1930
2174 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2233
1931 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1990
2234 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2293
1991 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2050
2294 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2353
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2354 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2413
2111 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2170
2414 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2473
2171 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2230
2474 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2533
2231 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2290
2534 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2593
2291 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2350
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2471 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2530
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TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-8383
 TELEFAX: (215) 568-5549
 TELEX: No. 5532340e
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3249 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US 08 429-264-1

Query Match 2.0% Score 68.2; DB 1; Length 3249;
 Best Local Similarity 53.0% Pred No 3 8e-07;
 Matches 170; Conservative 0; Mismatches 149; Indels 3; Gaps 1.

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DB 2609 ATAGAGGCTTTTGATAGAAAG 2869

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RESULTS 15
 US 08-832-883-1

Sequence 1: Application US/0883283
 Patent No. 5807681

GENERAL INFORMATION:
 APPLICANT: Giordano, Antonio

APPLICANT: Baldi, Alfonso

TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS

NUMBER OF SEQUENCES: 115

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.

STREET: Suite 1800 Two Penn Center Plaza

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOURCE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/842,883

FILING DATE:

CLASSIFICATION: 435

APPLICANT/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 8421-13 US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549
 INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4853 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 70..3489

US-08-832-883-1

Query Match 2.0% Score 68.2; DB 1; Length 4853;

Best Local Similarity 53.0% Pred No 4 6e-07;

Matches 170; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

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Search completed: January 17, 2003, 18:26:43

Job time: 126.421 secs

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CM nucleic acid search, using SW model

Run on: January 16, 2003, 15:20:22 : Search time 59.1896 seconds
(without alignments)

14944,909 Million cell updates/sec

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Perfect score: 3424

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Sequencing table: 10011111 N00

Gapop 10.0 : Gapext 1.0

Searches: 441362 seqs, 15000081 residues

Total number of hits satisfying chosen parameters: 862724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 90%

Maximum Match 100%

Listed first 45 summaries

Database: Issued Patents NA.*

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- 2: 2606.6.patdat/2104/56.COMB.seq.*
- 3: 2606.6.patdat/2104/56.COMB.seq.*
- 4: 2606.6.patdat/2104/56.COMB.seq.*
- 5: 2606.6.patdat/2104/56.COMB.seq.*
- 6: 2606.6.patdat/2104/56.COMB.seq.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	4224.6	97.3	4242	2	US-08 470 091 1
3	4224.4	97.0	4242	1	US-08 048-760 2
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5	2534	76.3	2994	1	US-08 203 429 2
6	2534	76.3	2994	2	US-08 482 627 4
7	2534	76.3	2994	3	US-08 801 092 3
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9	2534.4	76.2	2994	5	US-08 10457 1
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28 43.2 1.3 599 4 US-09 462 616A 202
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44 42.4 1.3 1186 2 US-08 741 722 5
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46 42 1.3 1864 4 US-09 406 293 4
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49 41.2 1.2 821 4 US-08 998 416 186
40 41.2 1.2 837 4 US-08 998 416 288
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43 40.6 1.2 4078 2 US-08 960 022 3
44 40.6 1.2 6265 4 US-09 129 112 3
45 40.6 1.2 12124 1 US-08 181 271A 46

ALPHABETICS

RESULT 1
US-08 048-760-1
Sequence 1, Application US/08048760
Patent No. 5496731

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji

APPLICANT: Hu, Shi Xue

APPLICANT: Benoit, L. William F.

TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and

Methods for Tumor Suppressor Gene Therapy.

TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edwards

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10046-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent In Release #1-0, Version #1.26

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/048,760

FILING DATE: 19990325

CLASSIFICATION: 424

AGENCY/AGENT INFORMATION:

NAME: FOISSANT, BRIAN M

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 7409 025 999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790 9000

TELEFAX: (212) 790 5711/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4242 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLGY: not relevant

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 19..2469

US-08-048-760-1

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Best local similarity: 99.9%, Prod. No. 92

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DB 694 AAATTCGATTTGAGTGTAAAGTTCCTGATGATGATGATGATGATGATGATGATGATGAT 752
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QY 590 AATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 629
DB 644 AATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 992
QY 630 AATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 689
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DB 1774 AATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1832
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QY 1590 TTTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1649
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DB 2254 TTTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2312
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DB 2734 TTTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2792

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that this is crucial for ensuring transparency and accountability in the organization's operations.

2. The second part of the document outlines the various methods and tools used to collect and analyze data. It highlights the need for a systematic approach to data collection and the importance of using reliable sources of information.

3. The third part of the document describes the process of interpreting the data and drawing conclusions from it. It stresses the importance of considering all relevant factors and avoiding biases in the analysis.

4. The fourth part of the document discusses the implications of the findings and the steps that should be taken to address any issues identified. It emphasizes the need for a proactive approach to problem-solving and the importance of continuous improvement.

5. The fifth part of the document provides a summary of the key points discussed and offers some final thoughts on the importance of maintaining accurate records and using data effectively.

Genome version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM nucleic nucleic search using sw model

Run on: January 16, 2003 15:20:22 : Search time 69.997 seconds
(without alignments)
14944.909 Million cell updates/sec

Filter: US 09 026 459A 46

Perfect score: 5377

Sequence: 1 GGGATGATGGGCGGAAAAA.....AAATGAGGATTAATGATAGT 4377

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Total number of hits satisfying chosen parameters: 98274

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

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 - 3: /seqz_6/ptdata/1/ina/6A_00MB.seq*
 - 4: /seqz_6/ptdata/1/ina/6A_00MB.seq*
 - 5: /seqz_6/ptdata/1/ina/6A_00MB.seq*
 - 6: /seqz_6/ptdata/1/ina/backfile1.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2852	84.5	3242	1	US 08 048 760 1
2	2852	84.5	3242	1	US 08 048 760 2
3	2852	84.5	3242	1	US 08 048 760 3
4	2852	84.5	3242	2	US 08 470 091 1
5	2852	84.5	3242	2	US 08 470 091 2
6	2490.6	73.8	2994	1	US 08 254 429 2
7	2490.6	73.8	2994	4	US 08 801 092 3
8	2489	73.7	2994	4	US 09 415 113 3
9	2487.4	73.7	2994	2	US 08 482 627 4
10	2487.4	73.7	2994	5	US 08 959 638 7
11	2486	73.6	2994	5	US 08 104 057 1
12	68.8	2.0	2808	1	US 08 428 673A 7
13	68.2	2.0	3249	1	US 07 708 962 1
14	68.2	2.0	3249	1	US 08 105 493A 1
15	68.2	2.0	4853	1	US 08 429 264 1
16	68.2	2.0	4853	2	US 08 852 883 1
17	65.6	1.9	2808	4	US 08 852 877 1
18	59	1.7	7218	1	US 08 152 7218 1
19	52	1.3	4747	4	US 08 242 463 14
20	44.6	1.3	1803	4	US 09 213 2940 2
21	44.6	1.3	15363	4	US 09 144 0010 799
22	44.4	1.3	23674	4	US 08 961 527 139
23	44	1.3	19124	2	US 09 431 638 651
24	43.8	1.3	1056	4	US 08 487 826B 13
25	43.2	1.3	509	4	US 09 144 0010 1550
26	43.2	1.3	509	4	US 09 432 607 202
27	43.2	1.3	509	4	US 09 432 607 202
28	43.2	1.3	509	4	US 09 432 607 202
29	43.2	1.3	509	4	US 09 432 607 202
30	43	1.3	5852	1	US 07 867 106 2
31	42.8	1.3	615	4	US 08 998 416 186
32	42.6	1.3	1189	1	US 08 407 591 2
33	42.4	1.3	2606	4	US 09 244 827B 3
34	42.4	1.3	1186	2	US 08 741 722 5
35	42.4	1.3	1174	2	US 08 741 722 5
36	42	1.2	645	2	US 08 893 795A 46
37	42	1.2	1864	4	US 09 468 265 4
38	41.8	1.2	1679	4	US 09 406 060 1
39	41.4	1.2	19124	2	US 08 487 826B 13
40	41.2	1.2	821	4	US 08 998 416 186
41	41.2	1.2	837	4	US 08 998 416 186
42	41.2	1.2	2038	2	US 08 254 429 2
43	40.8	1.2	1144	1	US 08 014 944A 1
44	40.8	1.2	1144	1	US 08 486 421 2
45	40.8	1.2	1144	1	US 08 470 911 2

ALIGNMENTS

RESULT 1
US-08-048-760-1
Sequence 1, Application US/08048760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Bi, Shi-Xue
TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and
METHODS FOR Tumor Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 4
REFERENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036, 2711
COMPUTER TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/048,760
FILING DATE: 19980325
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/RET NUMBER: 7409, 625,999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790 9090
TELEFAX: (212) 809 9741/8864
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3242 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19..2469
US-08-048-760-1

Query Match: 84.5%, Score: 2852, DB 1: Locust, 4242
Best Local Similarity: 94.4%, Pred. No. 0:
Matches: 4042, Conservative: 5, Mismatches: 177, Gaps: 1

874	3A'AGTTTTGAACA'AGAGACACAC'GAAAAAGTAACTTGTGATGAGAGGTGAATGTA	933
875	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
876	3A'AGTTTTGAACA'AGAGACACAC'GAAAAAGTAACTTGTGATGAGAGGTGAATGTA	786
877	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
878	ATT'ATGACAC'AC'CTGACCTTAGAG'CTGTATATGAAACACTATCCCAACAATTAAATGATGATT	993
879	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
880	ATT'ATGACAC'AC'CTGACCTTAGAG'CTGTATATGAAACACTATCCCAACAATTAAATGATGATT	846
881	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
882	TTAAATTCAGCAAGTATCAAGCTTCAGAAATCTGATTTGCTTAATTTAA'AA'CTGACA	906
883	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
884	GT'AAATCCAAAAGAAAATATATATGAAAA'ACTTGAAG'GATATAGATATAC'CTTTTAAAGAG	1113
885	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
886	GT'AAATCCAAAAGAAAATATATATGAAAA'ACTTGAAG'GATATAGATATAC'CTTTTAAAGAG	966
887	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
888	AAATTTCTTAAAG'CTGTGAG'AAAG'CTGTG'AAATTTGATCAGAGCATAC'AAACTT	1173
889	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
890	AAATTTCTTAAAG'CTGTGAG'AAAG'CTGTG'AAATTTGATCAGAGCATAC'AAACTT	1026
891	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
892	GAATCTGCTTTGTA'CAACCGATTAATGAATTCATGCTTAAATCAGAGAGAGAACCATTA	1233
893	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
894	GAATCTGCTTTGTA'CAACCGATTAATGAATTCATGCTTAAATCAGAGAGAGAACCATTA	1086
895	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
896	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1293
897	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
898	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1146
899	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
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901	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
902	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1206
903	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
904	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1413
905	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
906	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1266
907	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
908	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1473
909	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
910	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1326
911	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
912	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1533
913	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
914	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1486
915	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
916	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1593
917	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
918	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1446
919	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
920	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1653
921	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
922	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1506
923	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
924	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1713
925	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
926	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1566
927	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
928	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1773
929	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
930	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1626
931	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
932	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1833
933	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
934	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1686
935	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
936	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1893
937	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
938	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1746
939	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
940	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1953
941	TTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	
942	TT'ATTCCAAAATTTTAA'AA'CTTCTGAATSAACAACATTTTCAATATGCTCTTATTTAGAG	1806

[illegible]

SEQUENCE CHARACTERISTICS:
 LENGTH: 2408 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 HYDROPHOBIC: NO
 ANTI SENSE: NO
 DS 07 708 962-1

Query Match: 2.0% Score 68.4; DB 1; Length 2408;

Best Local Similarity: 53.0%; Pred. No. 4; 07;
 Matches 170; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

QY 1745 AAGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 1804
 DB 1940 AAGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 1999
 QY 1805 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 1864
 DB 2000 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2056
 QY 1865 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 1924
 DB 2057 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2116
 QY 1925 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 1984
 DB 2117 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2176
 QY 1985 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2044
 DB 2177 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2236
 QY 2045 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2104
 DB 2237 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2296

RESULT 13

US-08-106-494A-1

Sequence 1, Application US/08/106494A

Patent No. 5457049

GENERAL INFORMATION:

APPLICANT: Antonio Giordano

TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN PRB2"

TITLE OF INVENTION: RELATED GENE PRODUCTS, AND DNA ENCODING

TITLE OF INVENTION: THEREFOR

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Temple University of The Commonwealth

STREET: 406 University Services Building

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/106-494A

FILING DATE: August 12, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mullins, J.G.

REGISTRATION NUMBER: 43,073

REFERENCE/DOCKET NUMBER: 6056-188

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8484

TELEFAX: (215) 568-5549

TELEX: No. 5457049

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2408 base pairs

TYPE: nucleic acid

STRANDEDNESS: Single

TOPOLOGY: linear

US-08-106-494A-1

Query Match:

Best Local Similarity: 53.0%; Pred. No. 4; 07;

Matches 170; Conservative 0; Mismatches 148; Indels 4; Gaps 1;

QY 1745 AAGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 1804
 DB 2312 AAGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2371
 QY 1805 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 1864
 DB 2372 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2428
 QY 1865 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 1924
 DB 2429 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2488
 QY 1925 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 1984
 DB 2489 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2548
 QY 1985 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2044
 DB 2545 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2608
 QY 2045 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2104
 DB 2609 AATGAGCAATTAATACATGCTGCTTTTATAAAAGAGTATGCTAGCTT 2629

RESULT 14

US-08-429-264-1

Sequence 1, Application US/08/429264

Patent No. 5932440

GENERAL INFORMATION:

APPLICANT: Antonio Giordano

TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN

TITLE OF INVENTION: PRB2"

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seidel, Gonda, Lavorata & Monaco, P.C.

STREET: 1800 Two Penn Center Plaza

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/429-264

FILING DATE:

CLASSIFICATION: 540

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: August 12, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, D.A.

REGISTRATION NUMBER: 40,480

REFERENCE/DOCKET NUMBER: 6056-188

us-09-026-459a-44.rni

us-09-026-459a-44.rni

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us-09-026-459a-44.rni

us-09-026-459a-44.rni

us-09-026-459a-44.rni

us-09-026-459a-44.rni

Best local similarity 99.58; Pred. No. 0; Matches 2442; Conservative 0; Mismatches 11; Indels 0; Gaps 0;			
QY	417	ITATTCAGCAATATACACTAGCTATGTTATAGCATTAATGTTTCACCTGGACACCCGAGGC	376
DB	842	TTAAAGACCAATATAAAGACAGCTGTTATACCATTAATGGTTCCACCTGGACACCCGAGGC	901
QY	433	TAGCTCAGCAACAGCACTGCGACGATAGCAAAACAACTACAAAATACATACAGAATATATC	436
DB	902	TAGCTCAGCAACAGCACTGCGACGATAGCAAAACAACTACAAAATACATACAGAATATATC	961
QY	437	AAGTCTCTGTAAGACCAATAGCAATGTAATATAGATAGGCTGCAAAAATATTTTTCAAAA	496
DB	914	AAGTCTCTGTAAGACCAATAGCAATGTAATATAGATAGGCTGCAAAAATATTTTTCAAAA	1021
QY	447	ATTITATATCTTTTATGATATCTCTTGACCTGTGATCATCTAATGGATCTCCAGAGTTG	556
DB	1022	ATTITATATCTTTTATGATATCTCTTGACCTGTGATCATCTAATGGATCTCCAGAGTTG	1081
QY	557	AAAAATCTTTTAAACGATACCAACAAATTTATCTTTAAAAATAAAGATCTACATGCAAGAT	616
DB	1182	AAAAATCTTTTAAACGATACCAACAAATTTATCTTTAAAAATAAAGATCTACATGCAAGAT	1141
QY	617	TATTTTGAATCAATATAAATCTCTTCACACTGATCTATAGACAGTTTGTGAACACAGCA	676
DB	1142	TATTTTGAATCAATATAAATCTCTTCACACTGATCTATAGACAGTTTGTGAACACAGCA	1201
QY	677	TAAATCAATGAAATATAGCTTTGATGAGGAGTGATGTAATTTGCTGCACACACTCCAG	736
DB	1282	TAAATCAATGAAATATAGCTTTGATGAGGAGTGATGTAATTTGCTGCACACACTCCAG	1261
QY	737	TAGGACTGTTATGACACTATCCCAACATTAATGATGATGTTTAAATTCAGCAAGTATC	796
DB	1262	TAGGACTGTTATGACACTATCCCAACATTAATGATGATGTTTAAATTCAGCAAGTATC	1321
QY	797	AAATTCACAAAATCTGATTTCTATTTTAAACACTGCACACTGAAATCCCAAAACAAAGTA	856
DB	1322	AAATTCACAAAATCTGATTTCTATTTTAAACACTGCACACTGAAATCCCAAAACAAAGTA	1381
QY	857	TATGTAATAATGATGAGGATATATGATATATCTTTTAAAGAGAAATTTGCTAAAGCTGTG	916
DB	1382	TATGTAATAATGATGAGGATATATGATATATCTTTTAAAGAGAAATTTGCTAAAGCTGTG	1441
QY	917	TATAGGCTTTTCTGCAAAATGCAATACACAGCAATACAAACTTGGAGTTCGGCTGATTAAC	976
DB	1442	TATAGGCTTTTCTGCAAAATGCAATACACAGCAATACAAACTTGGAGTTCGGCTGATTAAC	1501
QY	977	TATTAATGCAATATATGCTTAAATTCAGAGAGCAATATATCCATTCAAAATTTTAGCA	1036
DB	1502	TATTAATGCAATATATGCTTAAATTCAGAGAGCAATATATCCATTCAAAATTTTAGCA	1061
QY	1037	TATTTCTGTAATGAAATTTTCTATATGCTTTTATTTGGGCTGGCTCTTGAGGTTGTAA	1096
DB	1502	TATTTCTGTAATGAAATTTTCTATATGCTTTTATTTGGGCTGGCTCTTGAGGTTGTAA	1621
QY	1097	TATTTCTGTAATGAAATTTTCTATATGCTTTTATTTGGGCTGGCTCTTGAGGTTGTAA	1156
DB	1622	TATTTCTGTAATGAAATTTTCTATATGCTTTTATTTGGGCTGGCTCTTGAGGTTGTAA	1681
QY	1157	TATGTAATGCAATATGCTTAAATTCAGAGAGCAATATATCCATTCAAAATTTTAGCA	1216
DB	1682	TATGTAATGCAATATGCTTAAATTCAGAGAGCAATATATCCATTCAAAATTTTAGCA	1741
QY	1217	TATTAATGCAATATGCTTAAATTCAGAGAGCAATATATCCATTCAAAATTTTAGCA	1276
DB	1742	TATTAATGCAATATGCTTAAATTCAGAGAGCAATATATCCATTCAAAATTTTAGCA	1801
QY	1277	TATTAATGCAATATGCTTAAATTCAGAGAGCAATATATCCATTCAAAATTTTAGCA	1336
DB	1802	TATTAATGCAATATGCTTAAATTCAGAGAGCAATATATCCATTCAAAATTTTAGCA	1861
QY	1337	TATTAATGCAATATGCTTAAATTCAGAGAGCAATATATCCATTCAAAATTTTAGCA	1396
DB	1862	TATTAATGCAATATGCTTAAATTCAGAGAGCAATATATCCATTCAAAATTTTAGCA	1931
QY	1397	CTCTCCAGCAATATACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG	1456
DB	1922	CTCTCCAGCAATATACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG	1981
QY	1457	AAAAAGCTTCAACATACCGTCTGTAATCTCTACAGCAAAATGCGACACACACCAATCTCAG	1516
DB	1982	AAAAAGCTTCAACATACCGTCTGTAATCTCTACAGCAAAATGCGACACACACCAATCTCAG	2041
QY	1517	CTCTCCAGCAATATACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG	1576
DB	2042	CTCTCCAGCAATATACACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG	2101
QY	1577	ATCTGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1636
DB	2102	ATCTGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2161
QY	1637	AATTAAGACATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1696
DB	2162	AATTAAGACATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2221
QY	1697	TGAGGACATAGCTTTTGGACCAATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1756
DB	2222	TGAGGACATAGCTTTTGGACCAATTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2281
QY	1757	AGATATATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1816
DB	2282	AGATATATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2341
QY	1817	TTCAGGACATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1876
DB	2342	TTCAGGACATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2401
QY	1877	TCTATATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1936
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QY	1937	GGGCGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1996
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QY	1997	CACCTTACGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2056
DB	2522	CACCTTACGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2581
QY	2057	TTCAGGACATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2116
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DB	2702	GGGCGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2761
QY	2237	TTCAGGACATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2296
DB	2762	TTCAGGACATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2821
QY	2297	GGGCGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2356
DB	2822	GGGCGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2881
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RESULT 7
 US 09 801 092 4
 Sequence 3: Application US/08031892
 Patent No. 6074850
 GENERAL INFORMATION
 APPLICANT: Andreiman, Douglas
 APPLICANT: Gregory, Richard J.
 APPLICANT: Wills, Kenneth N.
 TITLE OF INVENTION: Tissue Specific Expression of
 TITLE OF INVENTION: Retinoblastoma Protein
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESS: TOWNSEND and TOWNSEND and CPFW LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM pc compatible
 OPERATING SYSTEM: pc dos/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/060631 092
 FILING DATE: 14 FEB 1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/067751 517
 FILING DATE: 15 NOV 1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: FILLIS, Roger A.
 REGISTRATION NUMBER: 45,146
 REFERENCE/DOCKET NUMBER: 016940-001020
 TELEPHONE: 415-576-0250
 TELEFAX: 704-576-0400
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2994 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US 09 801 092 4

Query Match 67.6% Score 2145.4 DB 3: length 2994;
 Best Local Similarity 99.5% Pied No. 0;
 Matches 2142 Conservative 0 Mismatches 11 Indels 0 Gaps 0;
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 1142 TATTTTGGATCATGATAAAATCTTTCAGACATGATTTTACAGACATGATTTTACAAATATCA 1201
 677 GAAAT 746
 1202 CAAC 1261
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 1262 TTAGAGCTGTATGAAAT 1321
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 1502 GAGTAAATGAAATCTGATTTCTATTTTAAATCTGATTTCTATTTTAAATCTGATTTCT 1561
 1037 AATCTTCGAAATGAAATCTGATTTCTATTTTAAATCTGATTTCTATTTTAAATCTGAT 1096
 1562 AATCTTCGAAATGAAATCTGATTTCTATTTTAAATCTGATTTCTATTTTAAATCTGAT 1621
 1097 TGCGCAT 1156
 1622 TGCGCAT 1681
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 1922 CTCTCCAGAT 1981
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 1577 ATGATCATGAT 1636
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 1637 AATCAAGACAGAGGAAATCTGATTTCTATTTTAAATCTGATTTCTATTTTAAATCTGAT 1696
 2162 AATCAAGACAGAGGAAATCTGATTTCTATTTTAAATCTGATTTCTATTTTAAATCTGAT 2221
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us-09-026-459a-45.rni

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GenCode version 5.1.3

us-09-026-459a-45

January 18, 2003, 04:12:19 : Search time 45.4981 seconds
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5391.080 million cell updates/sec

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RESULT 2

US 09 482 627 4

Sequence 4, Application US/08482627

Patent No. 699434

GENERAL INFORMATION:

APPLICANT: Leu, Eva Y H P

APPLICANT: Leu, Eva Y H P

TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor

TITLE OF INVENTION: and Regulator

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

```

STREET: 4370 La Jolla Village Drive, Suite 100
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08 482 627
FILING DATE: 28 SEP 1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Carolyn A.
REGISTRATION NUMBER: 41,815
REFERENCE/DOCKET NUMBER: P 08 4737
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 545-9001
TELEFAX: (619) 545-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
NAME/KEY: CDS
LOCATION: 139..2924
US-08-482-627 4

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Alignment Scores:

Pred. No.: 0 Length: 2994

Score: 4068.50 Matches: 797

Percent Similarity: 85.88% Conservative: 0

Best Local Similarity: 85.88% Mismatches: 0

Query Match: 98.18% Indels: 131

DB: 2 Gaps: 1

US-09 026 459A 45 (1 797) x DS 08 482 627 4 (1 2994)

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QY 41 AsnProLeuValArgLeuGluPheGluThrGluLeuProAspThrAlaLeu 60
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Db 2779 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2838
QY 779 LeuAlaCysMetThrSerThrArgThrArgMetGluGluGluGluGluGlu 289
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QY 790 AspThrSerAsnLysGluLeuLys 797
Db 2899 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2922
RESULT 8
US-08-038-760-1
Sequence 1, Application US/08048740
Patent No. 5496741
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Xu, Hong-Xu
APPLICANT: Reed, William F.
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
METHODS OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Peunle & Edmunds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10046, 2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/338,760, 766
FILING DATE: 19940425
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-026-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9060
TELEFAX: (212) 863-9442/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3242 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
COMPLEXITY: not relevant
MOLECULE TYPE: DNA
FEATURES:
NAME/KEY: CDS
LOCATION: 19..2469
US-08-038-760-1
Alignment Scores:
Prod. No.: 0 Length: 4232
Score: 3556.00 Matches: 687
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 85.67% Indels: 0
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Db 406 GTGTTAT 405
QY 131 ArgAlaAlaLysSerGluGluGluGluGluGluGluGluGluGluGluGlu 190
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RESULT 12

US-09-026-459a-1

; Sequence 1, Application US/07708962

; Patent No. 5,262,921

; GENERAL INFORMATION:


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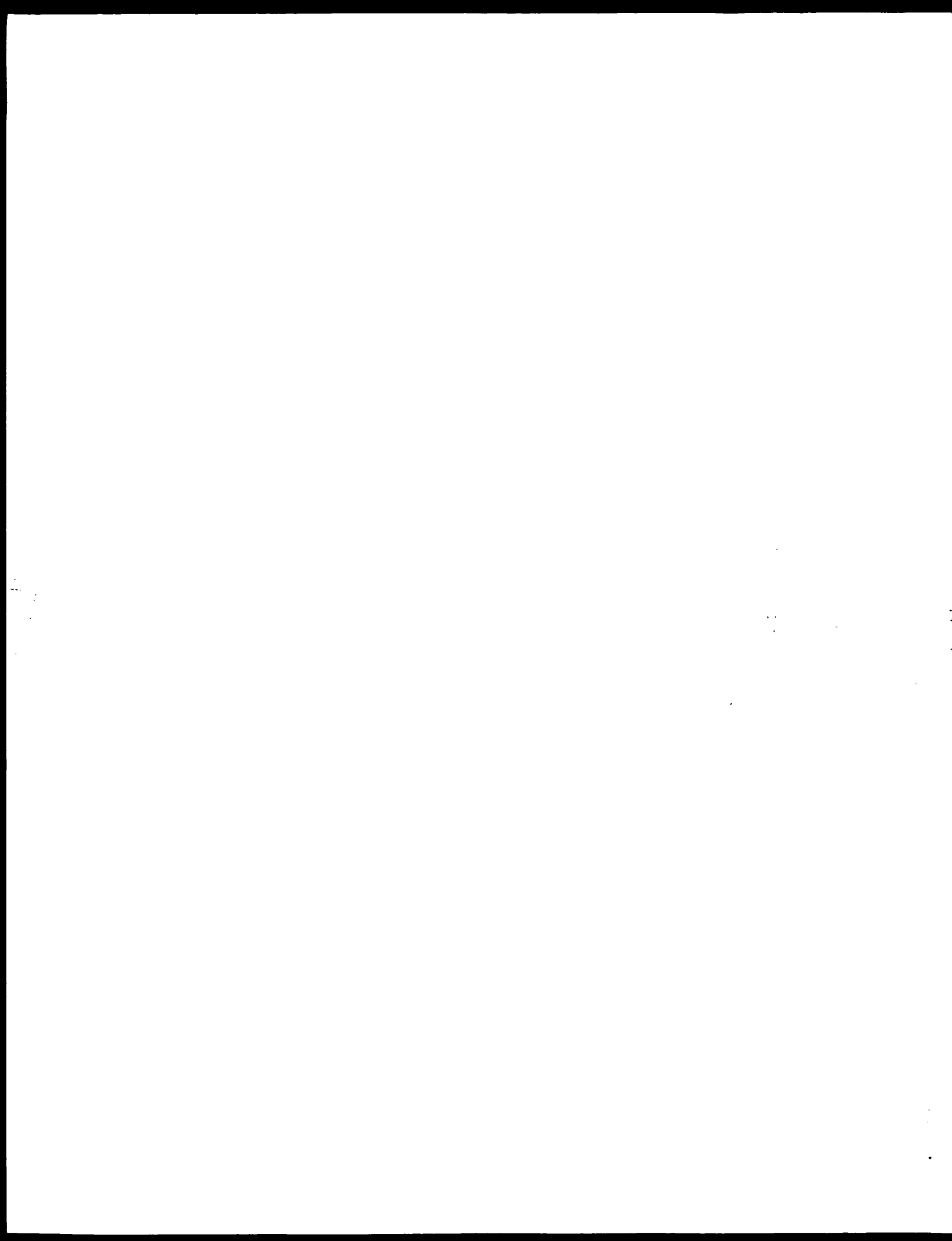
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 40 CysGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 111
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Genature version 5.1.4
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(without alignments)
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Scoring table: IDENTITY NUC

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Searched: 441662 seqs, 15330391 residues

Total number of hits satisfying chosen parameters: 88274

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4219.2	90.6	4242	1 US-08-038-760-2	Sequence 2, Appl
3	4219.2	90.6	4242	2 US-08-470-091-1	Sequence 1, Appl
4	4219.2	90.6	4242	2 US-08-470-091-2	Sequence 2, Appl
5	2857.8	80.4	2994	1 US-08-324-329-2	Sequence 2, Appl
6	2857.8	80.4	2994	3 US-08-801-092-3	Sequence 3, Appl
7	2857.8	80.4	2994	4 US-09-315-113-3	Sequence 3, Appl
8	2856.2	80.4	2994	2 US-08-482-627-4	Sequence 4, Appl
9	2854.8	80.3	2995	2 US-08-959-638-7	Sequence 7, Appl
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11	2853.2	80.3	2995	4 US-08-328-673A-7	Sequence 7, Appl
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18	59	1.7	7218	1 US-08-232-463-14	Sequence 14, Appl
19	51	1.4	3747	4 US-09-213-293D-2	Sequence 2, Appl
20	44.6	1.3	1803	4 US-09-134-001C-799	Sequence 799, App
21	44.6	1.3	15363	4 US-08-961-527-139	Sequence 139, App
22	44.4	1.2	29674	2 US-09-641-638-651	Sequence 651, App
23	44	1.2	19124	2 US-08-487-826B-13	Sequence 13, Appl
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33	42.6	1.2	2636	4 US-09-234-827H-4	Sequence 4, Appl
34	42.4	1.2	1185	2 US-08-731-722-5	Sequence 5, Appl
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37	42	1.2	1864	4 US-09-468-265-4	Sequence 4, Appl
38	41.8	1.2	1679	4 US-09-306-060-1	Sequence 1, Appl
39	41.4	1.2	19124	2 US-08-487-826H-13	Sequence 13, Appl
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ALIGNMENTS

RESULT 1
US-08-038-760-1
Sequence 1, Application US/08038760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Houq-Ji
APPLICANT: Benedict, William F.
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and Methods for Tumor Suppressor Gene Therapy.
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and Methods for Tumor Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/087048,760
FILING DATE: 1993/03/25
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fossant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409 025 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3242 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19..2469
US-08-038-760-1

Query Match: 96.0%, Score 4219.2, DB 1, Length 4242
Best local similarity: 99.9%, Pred. No. 0;
Matches 3221, Conservative 0; Mismatches 3; Gaps 0;

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QY 2551 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2610
DB 1011 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 951
QY 2611 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2670
DB 951 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 891
QY 2671 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2730
DB 891 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 831
QY 2731 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2790
DB 831 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
QY 2791 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2850
DB 771 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 711
QY 2851 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2910
DB 711 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
QY 2911 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2970
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QY 2971 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3030
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QY 3031 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3090
DB 531 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 471
QY 3091 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3150
DB 471 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
QY 3151 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3210
DB 411 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 351
QY 3211 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3270
DB 351 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 291
QY 3271 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3330
DB 291 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 231
QY 3331 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3390
DB 231 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 171
QY 3391 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3450
DB 171 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 111
QY 3451 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3510
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QY 3511 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3554
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